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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Croteau *et al.*

Application No.: _____

Filed: Herewith

Confirmation No.: _____

For: P450 OXYGENASES AND METHODS OF
USE

Examiner: _____

Art Unit: _____

Attorney Reference No.: 4630-66380-05

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STATEMENT IN COMPLIANCE WITH 37 C.F.R. § 1.821(f)

In compliance with 37 C.F.R. § 1.821(f), the undersigned declares that the nucleotide and/or amino acid sequences presented in the paper copy of the "Sequence Listing" submitted herewith are the same as the sequences contained in the computer-readable form of said "Sequence Listing." No new matter has been added.

Respectfully submitted,

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10/20/2003

SEQUENCE LISTING

AP20 Recd 18 JAN 2006

<110> Washington State University Research Foundation
Rodney, Croteau
Stefan, Jennewein
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<120> P450 OXYGENASES AND METHODS OF USE

<130> 4630-66380-05

<150> PCT/US2004/023656

<151> 2004-07-21

<150> US 60/489,597

<151> 2003-07-22

<160> 41

<170> PatentIn version 3.2

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Gly Asn Ser Phe Ala Asp Lys Glu Ile Leu Asp Asn Phe Ser Phe Leu
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Lys Leu Leu Ser Ser Ser Pro Glu Cys Tyr Glu Asn Ile Ala Gln Glu
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Gln Leu Glu Ile Leu Gly Asn Lys Lys Asp Arg Glu Glu Ile Ser Trp
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Pro Tyr Thr Phe Ile Pro Phe Gly Gly Gly Leu Arg Ile Cys Ala Gly
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Trp Glu Phe Ala Lys Met Glu Ile Leu Leu Phe Met His His Phe Val
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Lys Thr Phe Ser His Phe Ile Pro Val Asp Pro Asn Glu Lys Ile Ser
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Phe Phe Gly Asp Arg Met Lys Lys Phe Gly Lys Val Phe Lys Thr Ser
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Leu Ile Gly His Pro Thr Ile Val Leu Cys Gly Ser Ser Gly Asn Arg
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Phe Leu Leu Ser Asn Glu Glu Lys Leu Val Arg Met Phe Pro Pro Asn
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Ser Ser Ser Lys Leu Leu Gly Gln Asp Ser Val Leu Gly Lys Ile Gly
 115 120 125

Glu Glu His Arg Ile Val Arg Thr Ala Leu Ala Arg Cys Leu Gly Pro
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Gln Ala Leu Gln Asn Tyr Val Ser Lys Met Ser Ser Glu Ile Gln Arg
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His Ile Asn Gln Lys Trp Lys Gly Lys Gly Glu Val Lys Met Leu Pro
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Leu Ile Arg Ser Leu Val Phe Ser Ile Ala Thr Ser Leu Phe Phe Gly
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Ile Thr Asp Glu Gln Gln Gln Glu Arg Leu His His Leu Leu Glu Thr
 195 200 205

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 <212> PRT
 <213> Taxus cuspidata

<400> 8

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Val Thr Gln Leu Gln Ala Ser Pro Ala Ile Leu Ser Thr Ala Leu Thr
 20 25 30

Ala Ile Ala Gly Ile Ile Val Leu Leu Val Ile Thr Ser Lys Arg Arg
 35 40 45

Ser Ser Leu Lys Leu Pro Pro Gly Lys Leu Gly Leu Pro Phe Ile Gly
 50 55 60

Glu Thr Leu Glu Phe Val Lys Ala Leu Arg Ser Asp Thr Leu Arg Gln
 65 70 75 80

Phe Val Glu Glu Arg Glu Gly Lys Phe Gly Arg Val Phe Lys Thr Ser
 85 90 95

Leu Leu Gly Lys Pro Thr Val Ile Leu Cys Gly Pro Ala Gly Asn Arg
 100 105 110

Leu Val Leu Ser Asn Glu Glu Lys Leu Leu His Val Ser Trp Ser Ala
 115 120 125

Gln Ile Ala Arg Ile Leu Gly Leu Asn Ser Val Ala Val Lys Arg Gly
 130 135 140

Asp Asp His Arg Val Leu Arg Val Ala Leu Ala Gly Phe Leu Gly Ser
 145 150 155 160

Ala Gly Leu Gln Leu Tyr Ile Gly Lys Met Ser Ala Leu Ile Arg Asn
 165 170 175

His Ile Asn Glu Lys Trp Lys Gly Lys Asp Glu Val Asn Val Leu Ser
 180 185 190

Leu Val Arg Asp Leu Val Met Asp Asn Ser Ala Ile Leu Phe Phe Asn
 195 200 205

Ile Tyr Asp Lys Glu Arg Lys Gln Gln Leu His Glu Ile Leu Lys Ile
 210 215 220

Ile Leu Ala Ser His Phe Gly Ile Pro Leu Asn Ile Pro Gly Phe Leu
 225 230 235 240

Tyr Arg Lys Ala Leu Lys Gly Ser Leu Lys Arg Lys Lys Ile Leu Ser
 245 250 255

Ala Leu Leu Glu Lys Arg Lys Asp Glu Leu Arg Ser Arg Leu Ala Ser
 260 265 270

Ser Asn Gln Asp Leu Leu Ser Val Leu Leu Ser Phe Arg Asp Glu Arg
 275 280 285

Gly Lys Pro Leu Ser Asp Glu Ala Val Leu Asp Asn Cys Phe Ala Met
 290 295 300

Leu Asp Ala Ser Tyr Asp Thr Thr Thr Ser Gln Met Thr Leu Ile Leu
 305 310 315 320

Lys Met Leu Ser Ser Asn Pro Glu Cys Phe Glu Lys Val Val Gln Glu
 325 330 335

Gln Leu Glu Ile Ala Ser Asn Lys Lys Glu Gly Glu Glu Ile Thr Met
 340 345 350

Lys Asp Ile Lys Ala Met Lys Tyr Thr Trp Gln Val Leu Gln Glu Ser
 355 360 365

Leu Arg Met Leu Ser Pro Val Phe Gly Thr Leu Arg Lys Thr Met Asn
 370 375 380

Asp Ile Asn His Asp Gly Tyr Thr Ile Pro Lys Gly Trp Gln Val Val
 385 390 395 400

Trp Thr Thr Tyr Ser Thr His Gln Lys Asp Ile Tyr Phe Lys Gln Pro
 405 410 415

Asp Lys Phe Met Pro Ser Arg Phe Glu Glu Glu Asp Gly His Leu Asp
 420 425 430

Ala Tyr Thr Phe Val Pro Phe Gly Gly Gly Arg Arg Thr Cys Pro Gly
 435 440 445

Trp Glu Tyr Ala Lys Val Glu Ile Leu Leu Phe Leu His His Phe Val
 450 455 460

Lys Ala Phe Ser Gly Tyr Thr Pro Thr Asp Pro His Glu Arg Ile Cys
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Gly Tyr Pro Val Pro Leu Val Pro Val Lys Gly Phe Pro Ile Lys Leu
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Ile Ala Arg Ser
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 <213> Taxus cuspidata

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 cgacgatcct atgtgaatct cccccctgga aatttagggt tacctttcat tggcgagacg 180
 atacagttct tgggggcact tcagtcagaa aaaccccata catttttcga tgagagagtg 240


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<210> 10
<211> 500
<212> PRT
<213> Taxus cuspidata

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<223> Xaa can be any naturally occurring amino acid

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<220>
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<223> Xaa can be any naturally occurring amino acid

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<220>
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<222> (371)..(371)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (402)..(402)
<223> Xaa can be any naturally occurring amino acid

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Ser Pro Leu Ile Ile Ser Xaa Ala Ala Ala Leu Ala Ala Phe Leu Gly
          20          25          30

Ile Val Ile Phe Ser Ile Phe Ser Ser Thr Arg Arg Ser Tyr Val Asn
          35          40          45

Leu Pro Pro Gly Asn Leu Gly Leu Pro Phe Ile Gly Glu Thr Ile Gln
          50          55          60

Phe Leu Gly Ala Leu Gln Ser Glu Lys Pro His Thr Phe Phe Asp Glu
65          70          75          80

Arg Val Lys Lys Phe Gly Lys Val Phe Lys Thr Ser Leu Ile Gly Asp
          85          90          95

Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn Arg Leu Val Leu Ser
          100          105          110

Asn Glu Asp Lys Leu Val Gln Ser Ala Gly Pro Lys Ser Phe Leu Lys
          115          120          125

Leu Phe Gly Glu Asp Ser Val Ala Ala Lys Arg Glu Glu Ser His Arg
          130          135          140

Ile Leu Arg Ser Ala Leu Gly Arg Phe Leu Gly Pro His Ala Leu Gln
          145          150          155          160

Asn Tyr Ile Gly Lys Met Asn Ser Glu Met Gln Arg His Phe Asp Asp
          165          170          175

Lys Trp Lys Gly Lys Asp Glu Val Lys Val Leu Pro Leu Val Arg Gly
          180          185          190

Leu Ile Phe Ser Ile Ala Thr Ser Leu Phe Phe Asn Ile Asn Asp Asp
          195          200          205

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Arg Gln Arg Glu Gln Leu His Gly Leu Leu Asp Thr Ile Leu Val Gly
 210 215 220
 Ser Met Thr Ile Pro Leu Asn Ile Pro Gly Thr Leu Phe Arg Lys Ala
 225 230 235 240
 Val Lys Ala Arg Ala Lys Leu Asp Glu Ile Leu Phe Ala Leu Ile Glu
 245 250 255
 Asn Arg Arg Arg Glu Leu Arg Ser Gly Leu Asn Ser Gly Asn Gln Asp
 260 265 270
 Leu Leu Ser Ser Leu Leu Thr Phe Lys Asp Glu Lys Gly Asn Pro Leu
 275 280 285
 Thr Asp Lys Glu Ile Leu Asp Asn Phe Ser Val Met Leu His Ala Ser
 290 295 300
 Tyr Asp Thr Thr Val Ser Pro Thr Val Leu Ile Leu Lys Leu Leu Ala
 305 310 315 320
 Ser Asn Pro Glu Cys Tyr Glu Lys Val Val Gln Glu Gln Leu Gly Ile
 325 330 335
 Leu Ala Ser Lys Lys Glu Gly Glu Glu Val Asn Trp Lys Asp Leu Lys
 340 345 350
 Ala Met Pro Tyr Thr Trp Gln Ala Ile Gln Glu Pro Leu Xaa Ala Ala
 355 360 365
 Met Pro Xaa Ala Ala Gln Leu Leu Glu Cys Phe Glu Glu Leu Ser Leu
 370 375 380
 Ile Phe Ser Trp Lys Ala Ile Gln Phe Gln Lys Asp Gly Gln Leu Cys
 385 390 395 400
 Gly Xaa Ala Ala Leu Ile Val Asn Gly Arg Glu Glu Phe Phe Asn Glu
 405 410 415
 Pro Asp Lys Phe Lys Pro Ser Arg Phe Glu Glu Gly Lys Pro Leu Asp
 420 425 430
 Pro Tyr Thr Phe Ile Pro Phe Gly Ala Gly Val Arg Ile Cys Ala Gly
 435 440 445

Trp Glu Phe Ala Lys Ala Glu Leu Leu Leu Phe Val His Pro Phe Val
 450 455 460

Lys Asn Phe Ser Gly Cys Ile Ile Ile Asp Pro Asn Glu Lys Ile Ser
 465 470 475 480

Gly Asp Pro Phe Pro Pro Leu Pro Thr Ser Gly Gln Leu Met Lys Leu
 485 490 495

Ile Pro Arg Ser
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 <211> 1530
 <212> DNA
 <213> *Taxus cuspidata*

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 cgttctaaac gccgttcctc tgttggacta ccccaggga aattagggtta ccctttcatt 180
 ggcgagtcgt tactgttcct gaaggctctt cgatcaaaca cagttgaaca atttttggac 240
 gagagagtga agaatttcgg gaatgtcttc aagacgtcat taattgggca tccgacagta 300
 gttctctgcg ggccctgcagg aaaccggcta atcctggcga acgaggagaa gctgggtgcag 360
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 ggcaaggcc atatgatcat ccgctccgca ctgcaaggct ttttcagccc tgggtgctctg 480
 cagaaataca taggccaat gagtaaaaca atagaaaatc atattaatga gaaatggaag 540
 ggaaacgacc aagtgagtg agttgctttg gtaggagatc tcgtcttcga tatttcggcc 600
 tgtttgcttct tcaatataaa tgagaagcat gaacgggaac gactgtttga gcttttgag 660
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 tcttccaatc ccgaatgcta tgaaaaagta gttcaagagc aattggggat actttcgaat 1020
 aaattggaag gagacgaaat cacatggaaa gatgtgaaat ccatgaaata tacatggcaa 1080
 gtcgttcagg aaacgttacg attgtatccg tcaatttttg gatcatttcg ccaggccatc 1140
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tacacaacac atcccaagga aatgtatttc agtgagccgg agaaattcct gccttcgagg 1260
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 cgttcatgtc caggatggga attttcaaag atggagattt tactgtcggg gcatcatttt 1380
 gttaaaacat tcagcacctt caccacagtt gaccagcag aaataattgc aagagattcc 1440
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 <211> 509
 <212> PRT
 <213> Taxus cuspidata

<400> 12

Met Asp Val Phe Tyr Pro Leu Lys Ser Thr Val Ala Lys Phe Asn Glu
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Val Leu Pro Leu Leu Leu Phe Leu Arg Ser Lys Arg Arg Ser Ser Val
 35 40 45

Gly Leu Pro Pro Gly Lys Leu Gly Tyr Pro Phe Ile Gly Glu Ser Leu
 50 55 60

Leu Phe Leu Lys Ala Leu Arg Ser Asn Thr Val Glu Gln Phe Leu Asp
 65 70 75 80

Glu Arg Val Lys Asn Phe Gly Asn Val Phe Lys Thr Ser Leu Ile Gly
 85 90 95

His Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn Arg Leu Ile Leu
 100 105 110

Ala Asn Glu Glu Lys Leu Val Gln Met Ser Trp Pro Lys Ser Ser Met
 115 120 125

Lys Leu Met Gly Glu Lys Ser Ile Thr Ala Lys Arg Gly Glu Gly His
 130 135 140

Met Ile Ile Arg Ser Ala Leu Gln Gly Phe Phe Ser Pro Gly Ala Leu
 145 150 155 160

Gln Lys Tyr Ile Gly Gln Met Ser Lys Thr Ile Glu Asn His Ile Asn
 165 170 175
 Glu Lys Trp Lys Gly Asn Asp Gln Val Ser Val Val Ala Leu Val Gly
 180 185 190
 Asp Leu Val Phe Asp Ile Ser Ala Cys Leu Phe Phe Asn Ile Asn Glu
 195 200 205
 Lys His Glu Arg Glu Arg Leu Phe Glu Leu Leu Glu Ile Ile Ala Val
 210 215 220
 Gly Val Leu Ala Val Pro Val Asp Leu Pro Gly Phe Ala Tyr His Arg
 225 230 235 240
 Ala Leu Gln Ala Arg Ser Lys Leu Asn Ala Ile Leu Ser Gly Leu Ile
 245 250 255
 Glu Lys Arg Lys Met Asp Leu Ser Ser Gly Leu Ala Thr Ser Asn Gln
 260 265 270
 Asp Leu Leu Ser Val Phe Leu Thr Phe Lys Asp Asp Arg Gly Asn Pro
 275 280 285
 Cys Ser Asp Glu Glu Ile Leu Asp Asn Phe Ser Gly Leu Leu His Gly
 290 295 300
 Ser Tyr Asp Thr Thr Val Ser Ala Met Ala Cys Val Phe Lys Leu Leu
 305 310 315 320
 Ser Ser Asn Pro Glu Cys Tyr Glu Lys Val Val Gln Glu Gln Leu Gly
 325 330 335
 Ile Leu Ser Asn Lys Leu Glu Gly Asp Glu Ile Thr Trp Lys Asp Val
 340 345 350
 Lys Ser Met Lys Tyr Thr Trp Gln Val Val Gln Glu Thr Leu Arg Leu
 355 360 365
 Tyr Pro Ser Ile Phe Gly Ser Phe Arg Gln Ala Ile Thr Asp Ile His
 370 375 380
 Tyr Asn Gly Tyr Ile Ile Pro Lys Gly Trp Lys Leu Leu Trp Thr Pro
 385 390 395 400
 Tyr Thr Thr His Pro Lys Glu Met Tyr Phe Ser Glu Pro Glu Lys Phe


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<210> 14
<211> 502
<212> PRT
<213> Taxus cuspidata

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<220>
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<223> Xaa can be any naturally occurring amino acid

<400> 14

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Phe Ile Gln Phe Gln Ser Ser Pro Ala Val Leu Ser Leu Ser Leu Ile
20           25           30

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Thr Thr Ile Leu Gly Val Leu Leu Leu Trp Phe Phe Leu His Lys Asn
35           40           45

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Gly Ser Ser Val Thr Leu Pro Pro Gly Asn Leu Gly Phe Pro Phe Ile
50           55           60

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Gly Glu Thr Ile Pro Phe Leu Arg Ala Leu Arg Ser Glu Thr Pro Gln

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65		70		75		80									
Thr	Phe	Phe	Asp	Glu	Arg	Val	Lys	Lys	Phe	Gly	Val	Val	Phe	Lys	Thr
			85						90					95	
Arg	Ile	Val	Gly	His	Pro	Thr	Val	Val	Leu	Cys	Gly	Pro	Glu	Gly	Asn
			100					105					110		
Arg	Phe	Leu	Leu	Ser	Asn	Glu	Asp	Lys	Leu	Val	Gln	Ala	Ser	Leu	Pro
		115					120					125			
Asn	Ser	Ser	Glu	Lys	Leu	Ile	Gly	Lys	Tyr	Ser	Ile	Leu	Ser	Lys	Arg
	130					135					140				
Gly	Glu	Glu	His	Arg	Ile	Leu	Arg	Ala	Ala	Leu	Ala	Arg	Phe	Leu	Arg
145					150					155					160
Pro	Gln	Ala	Leu	Gln	Gly	Tyr	Val	Ala	Lys	Met	Ser	Ser	Glu	Ile	Gln
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His	His	Ile	Lys	Gln	Lys	Trp	Lys	Gly	Asn	Asp	Glu	Val	Lys	Val	Leu
			180					185					190		
Pro	Leu	Ile	Arg	Thr	Leu	Ile	Phe	Asn	Ile	Ala	Ser	Ser	Leu	Phe	Phe
		195					200					205			
Gly	Ile	Asn	Asp	Glu	His	Gln	Gln	Glu	Gln	Leu	His	His	Leu	Leu	Glu
	210					215					220				
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225					230					235					240
Arg	Phe	Arg	Lys	Ala	Leu	Asp	Ala	Arg	Ser	Lys	Leu	Asp	Glu	Ile	Leu
			245						250					255	
Ser	Ser	Leu	Met	Glu	Ser	Arg	Arg	Arg	Asp	Leu	Arg	Leu	Gly	Thr	Ala
			260					265					270		
Ser	Glu	Asn	Gln	Asp	Leu	Leu	Ser	Val	Leu	Leu	Thr	Phe	Lys	Asp	Glu
		275					280					285			
Arg	Gly	Asn	Pro	Leu	Thr	Asp	Lys	Glu	Ile	Phe	Asp	Asn	Phe	Ser	Phe
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Met	Leu	His	Ala	Ser	Tyr	Asp	Thr	Thr	Val	Ser	Pro	Thr	Gly	Leu	Met
305					310					315					320

Leu Lys Leu Leu Phe Ser Ser Pro Asp Cys Tyr Glu Lys Leu Val Gln
 325 330 335

Glu Gln Leu Gly Ile Val Gly Asn Lys Lys Glu Gly Glu Glu Ile Ser
 340 345 350

Trp Asn Asp Leu Lys Ala Met Lys Tyr Thr Cys Lys Val Val Gln Glu
 355 360 365

Ser Met Arg Met Leu Pro Pro Val Phe Gly Ser Tyr Arg Lys Ala Xaa
 370 375 380

Ala Ala Thr Tyr Ile His Tyr Asp Gly Tyr Thr Ile Pro Lys Gly Trp
 385 390 395 400

Asn Ile Phe Trp Ser Pro Tyr Thr Thr His Gly Lys Glu Glu Tyr Phe
 405 410 415

Asn Glu Ala Asp Lys Phe Met Pro Ser Arg Phe Glu Glu Gly Lys Tyr
 420 425 430

Val Ala Pro Tyr Thr Phe Leu Pro Phe Gly Ala Gly Leu Arg Val Cys
 435 440 445

Pro Gly Trp Glu Phe Ala Lys Thr Glu Ile Leu Leu Phe Val His His
 450 455 460

Phe Ile Thr Thr Phe Ser Ser Tyr Ile Pro Ile Asp Pro Lys Asp Lys
 465 470 475 480

Ile Ser Gly Asp Pro Phe Pro Pro Leu Pro Thr Asn Gly Phe Ser Met
 485 490 495

Lys Leu Phe Thr Arg Ser
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<210> 15
 <211> 1494
 <212> DNA
 <213> Taxus cuspidata

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actattcttg tgggaagttt gtcagtcccg ctggactttc caggaactcg ttatcgtaaa 720
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<210> 16
<211> 497
<212> PRT
<213> Taxus cuspidata

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<400> 16

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1           5           10          15

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Leu Glu Ser Ser Pro Ala Ile Leu Ser Leu Thr Leu Ala Pro Ile Leu
20           25           30

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Ala Ile Ile Leu Leu Leu Leu Phe Arg Tyr Asn His Arg Ser Ser Val
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 Lys Leu Pro Pro Gly Lys Leu Gly Phe Pro Leu Ile Gly Glu Thr Ile
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 65 70 75 80
 Asp Arg Leu Lys Lys Phe Gly Pro Val Tyr Met Thr Ser Leu Ile Gly
 85 90 95
 His Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn Lys Leu Val Leu
 100 105 110
 Ser Asn Glu Asp Lys Leu Val Glu Met Glu Gly Pro Lys Ser Phe Met
 115 120 125
 Lys Leu Ile Gly Glu Asp Ser Ile Val Ala Lys Arg Gly Glu Asp His
 130 135 140
 Arg Ile Leu Arg Thr Ala Leu Ala Arg Phe Leu Gly Ala Gln Ala Leu
 145 150 155 160
 Gln Asn Tyr Leu Gly Arg Met Ser Ser Glu Ile Gly His His Phe Asn
 165 170 175
 Glu Lys Trp Lys Gly Lys Asp Glu Val Lys Val Leu Pro Leu Val Arg
 180 185 190
 Gly Leu Ile Phe Ser Ile Ala Ser Thr Leu Phe Phe Asp Val Asn Asp
 195 200 205
 Gly His Gln Gln Lys Gln Leu His His Leu Leu Glu Thr Ile Leu Val
 210 215 220
 Gly Ser Leu Ser Val Pro Leu Asp Phe Pro Gly Thr Arg Tyr Arg Lys
 225 230 235 240
 Gly Leu Gln Ala Arg Leu Lys Leu Asp Glu Ile Leu Ser Ser Leu Ile
 245 250 255
 Lys Arg Arg Arg Arg Asp Leu Arg Ser Gly Ile Ala Ser Asp Asp Gln
 260 265 270
 Asp Leu Leu Ser Val Leu Leu Thr Phe Arg Asp Glu Lys Gly Asn Ser

275					280					285					
Leu	Thr	Asp	Gln	Gly	Ile	Leu	Asp	Asn	Phe	Ser	Ala	Met	Phe	His	Ala
290						295					300				
Ser	Tyr	Asp	Thr	Thr	Val	Ala	Pro	Met	Ala	Leu	Ile	Phe	Lys	Leu	Leu
305					310					315					320
Tyr	Ser	Asn	Pro	Glu	Tyr	His	Glu	Lys	Val	Phe	Gln	Glu	Gln	Leu	Glu
				325					330					335	
Ile	Ile	Gly	Asn	Lys	Lys	Glu	Gly	Glu	Glu	Ile	Ser	Trp	Lys	Asp	Leu
			340					345					350		
Lys	Ser	Met	Lys	Tyr	Thr	Trp	Gln	Ala	Val	Gln	Glu	Ser	Leu	Arg	Met
		355					360					365			
Tyr	Pro	Pro	Val	Phe	Gly	Ile	Phe	Arg	Lys	Ala	Ile	Thr	Asp	Ile	His
	370					375					380				
Tyr	Asp	Gly	Tyr	Thr	Ile	Pro	Lys	Gly	Trp	Arg	Val	Leu	Cys	Ser	Pro
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Tyr	Thr	Thr	His	Leu	Arg	Glu	Glu	Tyr	Phe	Pro	Glu	Pro	Glu	Glu	Phe
				405					410					415	
Arg	Pro	Ser	Arg	Phe	Glu	Asp	Glu	Gly	Arg	His	Val	Thr	Pro	Tyr	Thr
			420					425					430		
Tyr	Val	Pro	Phe	Gly	Gly	Gly	Leu	Arg	Thr	Cys	Pro	Gly	Trp	Glu	Phe
	435						440					445			
Ser	Lys	Ile	Glu	Ile	Leu	Leu	Phe	Val	His	His	Phe	Val	Lys	Asn	Phe
	450					455					460				
Ser	Ser	Tyr	Ile	Pro	Val	Asp	Pro	Asn	Glu	Lys	Val	Leu	Ser	Asp	Pro
465				470						475					480
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Ser															

<210> 17
 <211> 1458

<212> DNA
 <213> *Taxus cuspidata*

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 ggaaatctag gcttccctct ggttggggag acactgcagt tcgtgaggtc acttggtctg 180
 agcactccac agcagtttat tgaagagaga atgagcaa atgtgggatgt gttcaagact 240
 tccataatcg ggcacccac agtagtgctg tgtggacctg ccggaaccg gttggttctg 300
 tcgaacgaga acaagctggt gcagatgtca tggccgagct ccatgatgaa actcatcggc 360
 gaagattgtc tcggcggcaa aacgggagag cagcatcgga tcgtacgcgc tgcactaact 420
 cggtttttgg gtccctcaagc attgcagaat catttcgcta aaatgagctc gggaatccaa 480
 cgccacatca atgaaaaatg gaagggaaag gatgaggcca ctgtacttcc tttggtaaaa 540
 gacctgtct tctcgtcgc aagccgcttg ttttttggt taactgagga gcacctgcag 600
 gagcaacttc ataacttggt ggaagttatt cttgtgggat ctttttctgt tccactcaac 660
 attcccggat tcagttacca taaagcgatt caggcaaggg ccaccctcgc tgacatcatg 720
 acccatttga tagaaaagag gagaaatgag ctgcgtgcag gcactgcac tgagaatcaa 780
 gatttgctct ctgttttct cactttcact gacgaaaggg ggaattcact ggcggaacaag 840
 gagatcctcg acaacttttc tatgttactt catggatcat atgactccac caattcccca 900
 cttaccatgt tgattaaagt cttggcctcc catccagaaa gctatgaaaa agtgggtcaa 960
 gagcaatttg gaatactct caccaaaatg gagggagaag aaattgcttg gaaagacctg 1020
 aaggagatga aatattcatg gcaagttggt caggaaacat tgcgcatgta tcctccatt 1080
 tttggaacat ttgcgaaagc catcactgac attcattaca atggttatac aattccaaaa 1140
 ggatggaaac ttttatggac aacttacagt actcaaacca aggaagagta tttcaaggac 1200
 gccgatcaat tcaagccatc aagatttgag gaggaaggga agcatgtaac cccttacaca 1260
 tacttacctt tcggaggagg catgcgtgtt tgtccagggt gggaaatcgc caagatggag 1320
 acattactgt ttctccatca ttttggttaa gccttctctg ggttgaaggc aattgatcca 1380
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 ctctattcca gatcttaa 1458

<210> 18
 <211> 485
 <212> PRT
 <213> *Taxus cuspidata*

<400> 18

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 Thr Leu Ala Val Met Ala Gly Ile Ile Leu Phe Phe Arg Ser Lys Arg
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 His Ser Ser Val Lys Leu Pro Pro Gly Asn Leu Gly Phe Pro Leu Val
 35 40 45
 Gly Glu Thr Leu Gln Phe Val Arg Ser Leu Gly Ser Ser Thr Pro Gln
 50 55 60
 Gln Phe Ile Glu Glu Arg Met Ser Lys Phe Gly Asp Val Phe Lys Thr
 65 70 75 80
 Ser Ile Ile Gly His Pro Thr Val Val Leu Cys Gly Pro Ala Gly Asn
 85 90 95
 Arg Leu Val Leu Ser Asn Glu Asn Lys Leu Val Gln Met Ser Trp Pro
 100 105 110
 Ser Ser Met Met Lys Leu Ile Gly Glu Asp Cys Leu Gly Gly Lys Thr
 115 120 125
 Gly Glu Gln His Arg Ile Val Arg Ala Ala Leu Thr Arg Phe Leu Gly
 130 135 140
 Pro Gln Ala Leu Gln Asn His Phe Ala Lys Met Ser Ser Gly Ile Gln
 145 150 155 160
 Arg His Ile Asn Glu Lys Trp Lys Gly Lys Asp Glu Ala Thr Val Leu
 165 170 175
 Pro Leu Val Lys Asp Leu Val Phe Ser Val Ala Ser Arg Leu Phe Phe
 180 185 190
 Gly Ile Thr Glu Glu His Leu Gln Glu Gln Leu His Asn Leu Leu Glu
 195 200 205
 Val Ile Leu Val Gly Ser Phe Ser Val Pro Leu Asn Ile Pro Gly Phe
 210 215 220
 Ser Tyr His Lys Ala Ile Gln Ala Arg Ala Thr Leu Ala Asp Ile Met
 225 230 235 240

Thr His Leu Ile Glu Lys Arg Arg Asn Glu Leu Arg Ala Gly Thr Ala
 245 250 255
 Ser Glu Asn Gln Asp Leu Leu Ser Val Leu Leu Thr Phe Thr Asp Glu
 260 265 270
 Arg Gly Asn Ser Leu Ala Asp Lys Glu Ile Leu Asp Asn Phe Ser Met
 275 280 285
 Leu Leu His Gly Ser Tyr Asp Ser Thr Asn Ser Pro Leu Thr Met Leu
 290 295 300
 Ile Lys Val Leu Ala Ser His Pro Glu Ser Tyr Glu Lys Val Ala Gln
 305 310 315 320
 Glu Gln Phe Gly Ile Leu Ser Thr Lys Met Glu Gly Glu Glu Ile Ala
 325 330 335
 Trp Lys Asp Leu Lys Glu Met Lys Tyr Ser Trp Gln Val Val Gln Glu
 340 345 350
 Thr Leu Arg Met Tyr Pro Pro Ile Phe Gly Thr Phe Arg Lys Ala Ile
 355 360 365
 Thr Asp Ile His Tyr Asn Gly Tyr Thr Ile Pro Lys Gly Trp Lys Leu
 370 375 380
 Leu Trp Thr Thr Tyr Ser Thr Gln Thr Lys Glu Glu Tyr Phe Lys Asp
 385 390 395 400
 Ala Asp Gln Phe Lys Pro Ser Arg Phe Glu Glu Glu Gly Lys His Val
 405 410 415
 Thr Pro Tyr Thr Tyr Leu Pro Phe Gly Gly Gly Met Arg Val Cys Pro
 420 425 430
 Gly Trp Glu Phe Ala Lys Met Glu Thr Leu Leu Phe Leu His His Phe
 435 440 445
 Val Lys Ala Phe Ser Gly Leu Lys Ala Ile Asp Pro Asn Glu Lys Leu
 450 455 460
 Ser Gly Lys Pro Leu Pro Pro Leu Pro Val Asn Gly Leu Pro Ile Lys
 465 470 475 480
 Leu Tyr Ser Arg Ser


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<210> 19
<211> 2700
<212> DNA
<213> Taxus brevifolia
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<220>
<221> CDS
<222> (22)..(2610)
<223> coding sequence
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1 5 10																
aag atg aac gca ttg ggg aac aag gca atc cac gat cca acg aat tgc																99
Lys Met Asn Ala Leu Gly Asn Lys Ala Ile His Asp Pro Thr Asn Cys																
15 20 25																
aga gcc aaa tct gag cgc caa atg atg tgg gtt tgc tcc aga tca ggg																147
Arg Ala Lys Ser Glu Arg Gln Met Met Trp Val Cys Ser Arg Ser Gly																
30 35 40																
cga acc aga gta aaa atg tcg aga gga agt ggt ggt cct ggt cct gtc																195
Arg Thr Arg Val Lys Met Ser Arg Gly Ser Gly Gly Pro Gly Pro Val																
45 50 55																
gta atg atg agc agc agc act ggc act agc aag gtg gtt tcc gag act																243
Val Met Met Ser Ser Ser Thr Gly Thr Ser Lys Val Val Ser Glu Thr																
60 65 70																
tcc agt acc att gtg gat gat atc cct cga ctc tcc gcc aat tat cat																291
Ser Ser Thr Ile Val Asp Asp Ile Pro Arg Leu Ser Ala Asn Tyr His																
75 80 85 90																
ggc gat ctg tgg cac cac aat gtt ata caa act ctg gag aca ccg ttt																339
Gly Asp Leu Trp His His Asn Val Ile Gln Thr Leu Glu Thr Pro Phe																
95 100 105																
cgt gag agt tct act tac caa gaa cgg gca gat gag ctg gtt gtg aaa																387
Arg Glu Ser Ser Thr Tyr Gln Glu Arg Ala Asp Glu Leu Val Val Lys																
110 115 120																
att aaa gat atg ttc aat gcg ctc gga gac gga gat atc agt ccg tct																435
Ile Lys Asp Met Phe Asn Ala Leu Gly Asp Gly Asp Ile Ser Pro Ser																
125 130 135																
gca tac gac act gcg tgg gtg gcg agg ctg gcg acc att tcc tct gat																483
Ala Tyr Asp Thr Ala Trp Val Ala Arg Leu Ala Thr Ile Ser Ser Asp																
140 145 150																
gga tct gag aag cca cgg ttt cct cag gcc ctc aac tgg gtt ttc aac																531
Gly Ser Glu Lys Pro Arg Phe Pro Gln Ala Leu Asn Trp Val Phe Asn																
155 160 165 170																
aac cag ctc cag gat gga tcg tgg ggt atc gaa tcg cac ttt agt tta																579
Asn Gln Leu Gln Asp Gly Ser Trp Gly Ile Glu Ser His Phe Ser Leu																

175										180					185					
tgc	gat	cga	ttg	ctt	aac	acg	acc	aat	tct	gtt	atc	gcc	ctc	tcg	gtt	627				
Cys	Asp	Arg	Leu	Leu	Asn	Thr	Thr	Asn	Ser	Val	Ile	Ala	Leu	Ser	Val					
			190				195				200									
tgg	aaa	aca	ggg	cac	agc	caa	gta	caa	caa	ggg	gct	gag	ttt	att	gca	675				
Trp	Lys	Thr	Gly	His	Ser	Gln	Val	Gln	Gln	Gly	Ala	Glu	Phe	Ile	Ala					
			205				210				215									
gag	aat	cta	aga	tta	ctc	aat	gag	gaa	gat	gag	ttg	tcc	ccg	gat	ttc	723				
Glu	Asn	Leu	Arg	Leu	Leu	Asn	Glu	Glu	Asp	Glu	Leu	Ser	Pro	Asp	Phe					
			220				225				230									
caa	ata	atc	ttt	cct	gct	ctg	ctg	caa	aag	gca	aaa	gcg	ttg	ggg	atc	771				
Gln	Ile	Ile	Phe	Pro	Ala	Leu	Leu	Gln	Lys	Ala	Lys	Ala	Leu	Gly	Ile					
			235				240				245				250					
aat	ctt	cct	tac	gat	ctt	cca	ttt	atc	aaa	tat	ttg	tcg	aca	aca	cgg	819				
Asn	Leu	Pro	Tyr	Asp	Leu	Pro	Phe	Ile	Lys	Tyr	Leu	Ser	Thr	Thr	Arg					
			255				260				265									
gaa	gcc	agg	ctt	aca	gat	gtt	tct	gcg	gca	gca	gac	aat	att	cca	gcc	867				
Glu	Ala	Arg	Leu	Thr	Asp	Val	Ser	Ala	Ala	Ala	Asp	Asn	Ile	Pro	Ala					
			270				275				280									
aac	atg	ttg	aat	gcg	ttg	gaa	ggg	ctc	gag	gaa	gtt	att	gac	tgg	aac	915				
Asn	Met	Leu	Asn	Ala	Leu	Glu	Gly	Leu	Glu	Glu	Val	Ile	Asp	Trp	Asn					
			285				290				295									
aag	att	atg	agg	ttt	caa	agt	aaa	gat	gga	tct	ttc	ctg	agc	tcc	cct	963				
Lys	Ile	Met	Arg	Phe	Gln	Ser	Lys	Asp	Gly	Ser	Phe	Leu	Ser	Ser	Pro					
			300				305				310									
gcc	tcc	act	gcc	tgt	gta	ctg	atg	aat	aca	ggg	gac	gaa	aaa	tgt	ttc	1011				
Ala	Ser	Thr	Ala	Cys	Val	Leu	Met	Asn	Thr	Gly	Asp	Glu	Lys	Cys	Phe					
			315				320				325				330					
act	ttt	ctc	aac	aat	ctg	ctc	gac	aaa	ttc	ggc	ggc	tgc	gtg	ccc	tgt	1059				
Thr	Phe	Leu	Asn	Asn	Leu	Leu	Asp	Lys	Phe	Gly	Gly	Cys	Val	Pro	Cys					
			335				340				345									
atg	tat	tcc	atc	gat	ctg	ctg	gaa	cgc	ctt	tcg	ctg	gtt	gat	aac	att	1107				
Met	Tyr	Ser	Ile	Asp	Leu	Leu	Glu	Arg	Leu	Ser	Leu	Val	Asp	Asn	Ile					
			350				355				360									
gag	cat	ctc	gga	atc	ggg	cgc	cat	ttc	aaa	caa	gaa	atc	aaa	gga	gct	1155				
Glu	His	Leu	Gly	Ile	Gly	Arg	His	Phe	Lys	Gln	Glu	Ile	Lys	Gly	Ala					
			365				370				375									
ctt	gat	tat	gtc	tac	aga	cat	tgg	agt	gaa	agg	ggc	atc	ggg	tgg	ggc	1203				
Leu	Asp	Tyr	Val	Tyr	Arg	His	Trp	Ser	Glu	Arg	Gly	Ile	Gly	Trp	Gly					
			380				385				390									
aga	gac	agc	ctt	gtt	cca	gat	ctc	aac	acc	aca	gcc	ctc	ggc	ctg	cga	1251				
Arg	Asp	Ser	Leu	Val	Pro	Asp	Leu	Asn	Thr	Thr	Ala	Leu	Gly	Leu	Arg					
			395				400				405				410					
act	ctt	cgc	atg	cac	gga	tac	aat	gtt	tct	tca	gac	gtt	ttg	aat	aat	1299				
Thr	Leu	Arg	Met	His	Gly	Tyr	Asn	Val	Ser	Ser	Asp	Val	Leu	Asn	Asn					
			415				420				425									

ttc aaa gat gaa aac ggg cgg ttc ttc tcc tct gcg ggc caa acc cat	1347
Phe Lys Asp Glu Asn Gly Arg Phe Phe Ser Ser Ala Gly Gln Thr His	
430 435 440	
gtc gaa ttg aga agc gtg gtg aat ctt ttc aga gct tcc gac ctt gca	1395
Val Glu Leu Arg Ser Val Val Asn Leu Phe Arg Ala Ser Asp Leu Ala	
445 450 455	
ttt cct gac gaa aga gct atg gac gat gct aga aaa ttt gca gaa cca	1443
Phe Pro Asp Glu Arg Ala Met Asp Asp Ala Arg Lys Phe Ala Glu Pro	
460 465 470	
tat ctt aga gag gca ctt gca acg aaa atc tca acc aat aca aaa cta	1491
Tyr Leu Arg Glu Ala Leu Ala Thr Lys Ile Ser Thr Asn Thr Lys Leu	
475 480 485 490	
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Phe Lys Glu Ile Glu Tyr Val Val Glu Tyr Pro Trp His Met Ser Ile	
495 500 505	
cca cgc tta gaa gcc aga agt tat att gat tca tat gac gac aat tat	1587
Pro Arg Leu Glu Ala Arg Ser Tyr Ile Asp Ser Tyr Asp Asp Asn Tyr	
510 515 520	
gta tgg cag agg aag act cta tat aga atg cca tct ttg agt aat tca	1635
Val Trp Gln Arg Lys Thr Leu Tyr Arg Met Pro Ser Leu Ser Asn Ser	
525 530 535	
aaa tgt tta gaa ttg gca aaa ttg gac ttc aat atc gta caa tct ttg	1683
Lys Cys Leu Glu Leu Ala Lys Leu Asp Phe Asn Ile Val Gln Ser Leu	
540 545 550	
cat caa gag gag ttg aag ctt cta aca aga tgg tgg aag gaa tcc ggc	1731
His Gln Glu Glu Leu Lys Leu Leu Thr Arg Trp Trp Lys Glu Ser Gly	
555 560 565 570	
atg gca gat ata aat ttc act cga cac cga gtg gcg gag gtt tat ttt	1779
Met Ala Asp Ile Asn Phe Thr Arg His Arg Val Ala Glu Val Tyr Phe	
575 580 585	
tca tca gct aca ttt gaa ccc gaa tat tct gcc act aga att gcc ttc	1827
Ser Ser Ala Thr Phe Glu Pro Glu Tyr Ser Ala Thr Arg Ile Ala Phe	
590 595 600	
aca aaa att ggt tgt tta caa gtc ctt ttt gat gat atg gct gac atc	1875
Thr Lys Ile Gly Cys Leu Gln Val Leu Phe Asp Asp Met Ala Asp Ile	
605 610 615	
ttt gca aca cta gat gaa ttg aaa agt ttc act gag gga gta aag aga	1923
Phe Ala Thr Leu Asp Glu Leu Lys Ser Phe Thr Glu Gly Val Lys Arg	
620 625 630	
tgg gat aca tct ttg cta cat gag att cca gag tgt atg caa act tgc	1971
Trp Asp Thr Ser Leu Leu His Glu Ile Pro Glu Cys Met Gln Thr Cys	
635 640 645 650	
ttt aaa gtt tgg ttc aaa tta atg gaa gaa gta aat aat gat gtg gtt	2019
Phe Lys Val Trp Phe Lys Leu Met Glu Glu Val Asn Asn Asp Val Val	
655 660 665	

aag gta caa gga cgt gac atg ctc gct cac ata aga aaa ccc tgg gag Lys Val Gln Gly Arg Asp Met Leu Ala His Ile Arg Lys Pro Trp Glu 670 675 680	2067
ttg tac ttc aat tgt tat gta caa gaa agg gag tgg ctt gaa gcc ggg Leu Tyr Phe Asn Cys Tyr Val Gln Glu Arg Glu Trp Leu Glu Ala Gly 685 690 695	2115
tat ata cca act ttt gaa gag tac tta aag act tat gct ata tca gta Tyr Ile Pro Thr Phe Glu Glu Tyr Leu Lys Thr Tyr Ala Ile Ser Val 700 705 710	2163
ggc ctt gga ccg tgt acc cta caa cca ata cta cta atg ggt gag ctt Gly Leu Gly Pro Cys Thr Leu Gln Pro Ile Leu Leu Met Gly Glu Leu 715 720 725 730	2211
gtg aaa gat gat gtt gtt gag aaa gtg cac tat ccc tca aat atg ttt Val Lys Asp Asp Val Val Glu Lys Val His Tyr Pro Ser Asn Met Phe 735 740 745	2259
gag ctt gta tcc ttg agc tgg cga cta aca aac gac acc aaa aca tat Glu Leu Val Ser Leu Ser Trp Arg Leu Thr Asn Asp Thr Lys Thr Tyr 750 755 760	2307
cag gct gaa aag gct cga gga caa caa gcc tca ggc ata gca tgc tat Gln Ala Glu Lys Ala Arg Gly Gln Gln Ala Ser Gly Ile Ala Cys Tyr 765 770 775	2355
atg aag gat aat cca gga gca act gag gaa gat gcc att aag cac ata Met Lys Asp Asn Pro Gly Ala Thr Glu Glu Asp Ala Ile Lys His Ile 780 785 790	2403
tgt cgt gtt gtt gat cgg gcc ttg aaa gaa gca agc ttt gaa tat ttc Cys Arg Val Val Asp Arg Ala Leu Lys Glu Ala Ser Phe Glu Tyr Phe 795 800 805 810	2451
aaa cca tcc aat gat atc cca atg ggt tgc aag tcc ttt att ttt aac Lys Pro Ser Asn Asp Ile Pro Met Gly Cys Lys Ser Phe Ile Phe Asn 815 820 825	2499
ctt aga ttg tgt gtc caa atc ttt tac aag ttt ata gat ggg tac gga Leu Arg Leu Cys Val Gln Ile Phe Tyr Lys Phe Ile Asp Gly Tyr Gly 830 835 840	2547
atc gcc aat gag gag att aag gac tat ata aga aaa gtt tat att gat Ile Ala Asn Glu Glu Ile Lys Asp Tyr Ile Arg Lys Val Tyr Ile Asp 845 850 855	2595
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<210> 20
 <211> 862
 <212> PRT
 <213> *Taxus brevifolia*
 <400> 20

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 Gln Met Met Trp Val Cys Ser Arg Ser Gly Arg Thr Arg Val Lys Met
 35 40 45
 Ser Arg Gly Ser Gly Gly Pro Gly Pro Val Val Met Met Ser Ser Ser
 50 55 60
 Thr Gly Thr Ser Lys Val Val Ser Glu Thr Ser Ser Thr Ile Val Asp
 65 70 75 80
 Asp Ile Pro Arg Leu Ser Ala Asn Tyr His Gly Asp Leu Trp His His
 85 90 95
 Asn Val Ile Gln Thr Leu Glu Thr Pro Phe Arg Glu Ser Ser Thr Tyr
 100 105 110
 Gln Glu Arg Ala Asp Glu Leu Val Val Lys Ile Lys Asp Met Phe Asn
 115 120 125
 Ala Leu Gly Asp Gly Asp Ile Ser Pro Ser Ala Tyr Asp Thr Ala Trp
 130 135 140
 Val Ala Arg Leu Ala Thr Ile Ser Ser Asp Gly Ser Glu Lys Pro Arg
 145 150 155 160
 Phe Pro Gln Ala Leu Asn Trp Val Phe Asn Asn Gln Leu Gln Asp Gly
 165 170 175
 Ser Trp Gly Ile Glu Ser His Phe Ser Leu Cys Asp Arg Leu Leu Asn
 180 185 190
 Thr Thr Asn Ser Val Ile Ala Leu Ser Val Trp Lys Thr Gly His Ser
 195 200 205
 Gln Val Gln Gln Gly Ala Glu Phe Ile Ala Glu Asn Leu Arg Leu Leu
 210 215 220
 Asn Glu Glu Asp Glu Leu Ser Pro Asp Phe Gln Ile Ile Phe Pro Ala
 225 230 235 240

485								490				495			
Val	Val	Glu	Tyr	Pro	Trp	His	Met	Ser	Ile	Pro	Arg	Leu	Glu	Ala	Arg
500								505				510			
Ser	Tyr	Ile	Asp	Ser	Tyr	Asp	Asp	Asn	Tyr	Val	Trp	Gln	Arg	Lys	Thr
515								520				525			
Leu	Tyr	Arg	Met	Pro	Ser	Leu	Ser	Asn	Ser	Lys	Cys	Leu	Glu	Leu	Ala
530								535				540			
Lys	Leu	Asp	Phe	Asn	Ile	Val	Gln	Ser	Leu	His	Gln	Glu	Glu	Leu	Lys
545								550				555			
Leu	Leu	Thr	Arg	Trp	Trp	Lys	Glu	Ser	Gly	Met	Ala	Asp	Ile	Asn	Phe
565								570				575			
Thr	Arg	His	Arg	Val	Ala	Glu	Val	Tyr	Phe	Ser	Ser	Ala	Thr	Phe	Glu
580								585				590			
Pro	Glu	Tyr	Ser	Ala	Thr	Arg	Ile	Ala	Phe	Thr	Lys	Ile	Gly	Cys	Leu
595								600				605			
Gln	Val	Leu	Phe	Asp	Asp	Met	Ala	Asp	Ile	Phe	Ala	Thr	Leu	Asp	Glu
610								615				620			
Leu	Lys	Ser	Phe	Thr	Glu	Gly	Val	Lys	Arg	Trp	Asp	Thr	Ser	Leu	Leu
625								630				635			
His	Glu	Ile	Pro	Glu	Cys	Met	Gln	Thr	Cys	Phe	Lys	Val	Trp	Phe	Lys
645								650				655			
Leu	Met	Glu	Glu	Val	Asn	Asn	Asp	Val	Val	Lys	Val	Gln	Gly	Arg	Asp
660								665				670			
Met	Leu	Ala	His	Ile	Arg	Lys	Pro	Trp	Glu	Leu	Tyr	Phe	Asn	Cys	Tyr
675								680				685			
Val	Gln	Glu	Arg	Glu	Trp	Leu	Glu	Ala	Gly	Tyr	Ile	Pro	Thr	Phe	Glu
690								695				700			
Glu	Tyr	Leu	Lys	Thr	Tyr	Ala	Ile	Ser	Val	Gly	Leu	Gly	Pro	Cys	Thr
705								710				715			
Leu	Gln	Pro	Ile	Leu	Leu	Met	Gly	Glu	Leu	Val	Lys	Asp	Asp	Val	Val
725								730				735			

Leu Leu Gln Lys Ala Lys Ala Leu Gly Ile Asn Leu Pro Tyr Asp Leu
 245 250 255

Pro Phe Ile Lys Tyr Leu Ser Thr Thr Arg Glu Ala Arg Leu Thr Asp
 260 265 270

Val Ser Ala Ala Ala Asp Asn Ile Pro Ala Asn Met Leu Asn Ala Leu
 275 280 285

Glu Gly Leu Glu Glu Val Ile Asp Trp Asn Lys Ile Met Arg Phe Gln
 290 295 300

Ser Lys Asp Gly Ser Phe Leu Ser Ser Pro Ala Ser Thr Ala Cys Val
 305 310 315 320

Leu Met Asn Thr Gly Asp Glu Lys Cys Phe Thr Phe Leu Asn Asn Leu
 325 330 335

Leu Asp Lys Phe Gly Gly Cys Val Pro Cys Met Tyr Ser Ile Asp Leu
 340 345 350

Leu Glu Arg Leu Ser Leu Val Asp Asn Ile Glu His Leu Gly Ile Gly
 355 360 365

Arg His Phe Lys Gln Glu Ile Lys Gly Ala Leu Asp Tyr Val Tyr Arg
 370 375 380

His Trp Ser Glu Arg Gly Ile Gly Trp Gly Arg Asp Ser Leu Val Pro
 385 390 395 400

Asp Leu Asn Thr Thr Ala Leu Gly Leu Arg Thr Leu Arg Met His Gly
 405 410 415

Tyr Asn Val Ser Ser Asp Val Leu Asn Asn Phe Lys Asp Glu Asn Gly
 420 425 430

Arg Phe Phe Ser Ser Ala Gly Gln Thr His Val Glu Leu Arg Ser Val
 435 440 445

Val Asn Leu Phe Arg Ala Ser Asp Leu Ala Phe Pro Asp Glu Arg Ala
 450 455 460

Met Asp Asp Ala Arg Lys Phe Ala Glu Pro Tyr Leu Arg Glu Ala Leu
 465 470 475 480

Ala Thr Lys Ile Ser Thr Asn Thr Lys Leu Phe Lys Glu Ile Glu Tyr

Glu Lys Val His Tyr Pro Ser Asn Met Phe Glu Leu Val Ser Leu Ser
740 745 750

Trp Arg Leu Thr Asn Asp Thr Lys Thr Tyr Gln Ala Glu Lys Ala Arg
755 760 765

Gly Gln Gln Ala Ser Gly Ile Ala Cys Tyr Met Lys Asp Asn Pro Gly
770 775 780

Ala Thr Glu Glu Asp Ala Ile Lys His Ile Cys Arg Val Val Asp Arg
785 790 795 800

Ala Leu Lys Glu Ala Ser Phe Glu Tyr Phe Lys Pro Ser Asn Asp Ile
805 810 815

Pro Met Gly Cys Lys Ser Phe Ile Phe Asn Leu Arg Leu Cys Val Gln
820 825 830

Ile Phe Tyr Lys Phe Ile Asp Gly Tyr Gly Ile Ala Asn Glu Glu Ile
835 840 845

Lys Asp Tyr Ile Arg Lys Val Tyr Ile Asp Pro Ile Gln Val
850 855 860

<210> 21
<211> 1419
<212> DNA
<213> Taxus cuspidata

<220>
<221> CDS
<222> (11)..(1330)
<223> coding sequence

<400> 21
cacagttaga atg gag aag aca gat tta cac gta aat ctg att gag aaa 49
Met Glu Lys Thr Asp Leu His Val Asn Leu Ile Glu Lys
1 5 10

gtg atg gtt ggg cca tcc ccg cct ctg ccc aaa acc acc ctg caa ctc 97
Val Met Val Gly Pro Ser Pro Pro Leu Pro Lys Thr Thr Leu Gln Leu
15 20 25

tcc tcc ata gac aac ctg cca ggg gta aga gga agc att ttc aat gcc 145
Ser Ser Ile Asp Asn Leu Pro Gly Val Arg Gly Ser Ile Phe Asn Ala
30 35 40 45

ttg tta att tac aat gcc tct ccc tct ccc acc atg atc tct gca gat 193
Leu Leu Ile Tyr Asn Ala Ser Pro Ser Pro Thr Met Ile Ser Ala Asp
50 55 60

cct gca aaa cca att aga gaa gct ctc gcc aag atc ctg gtt tat tat	241
Pro Ala Lys Pro Ile Arg Glu Ala Leu Ala Lys Ile Leu Val Tyr Tyr	
65 70 75	
ccc cct ttt gct ggg cgc ctc aga gag aca gaa aat ggg gat ctg gaa	289
Pro Pro Phe Ala Gly Arg Leu Arg Glu Thr Glu Asn Gly Asp Leu Glu	
80 85 90	
gtg gaa tgc aca ggg gag ggt gct atg ttt ttg gaa gcc atg gca gac	337
Val Glu Cys Thr Gly Glu Gly Ala Met Phe Leu Glu Ala Met Ala Asp	
95 100 105	
aat gag ctg tct gtg ttg gga gat ttt gat gac agc aat cca tca ttt	385
Asn Glu Leu Ser Val Leu Gly Asp Phe Asp Asp Ser Asn Pro Ser Phe	
110 115 120 125	
cag cag cta ctt ttt tcg ctt cca ctc gat acc aat ttc aaa gac ctc	433
Gln Gln Leu Leu Phe Ser Leu Pro Leu Asp Thr Asn Phe Lys Asp Leu	
130 135 140	
tct ctt ctg gtt gtt cag gta act cgt ttt aca tgt gga ggc ttt gtt	481
Ser Leu Leu Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val	
145 150 155	
gtt gga gtg agt ttc cac cat ggt gta tgt gat ggt cga gga gcg gcc	529
Val Gly Val Ser Phe His His Gly Val Cys Asp Gly Arg Gly Ala Ala	
160 165 170	
caa ttt ctt aaa ggt ttg gca gag atg gca cgg gga gag gtt aag ctc	577
Gln Phe Leu Lys Gly Leu Ala Glu Met Ala Arg Gly Glu Val Lys Leu	
175 180 185	
tca ttg gaa cca ata tgg aat agg gaa cta gtg aag ctt gat gac cct	625
Ser Leu Glu Pro Ile Trp Asn Arg Glu Leu Val Lys Leu Asp Asp Pro	
190 195 200 205	
aaa tac ctt caa ttt ttt cac ttt gaa ttc cta cga gcg cct tca att	673
Lys Tyr Leu Gln Phe Phe His Phe Glu Phe Leu Arg Ala Pro Ser Ile	
210 215 220	
gtt gag aaa att gtt caa aca tat ttt att ata gat ttt gag acc ata	721
Val Glu Lys Ile Val Gln Thr Tyr Phe Ile Ile Asp Phe Glu Thr Ile	
225 230 235	
aat tat atc aaa caa tct gtt atg gaa gaa tgt aaa gaa ttt tgc tct	769
Asn Tyr Ile Lys Gln Ser Val Met Glu Glu Cys Lys Glu Phe Cys Ser	
240 245 250	
tca ttc gaa gtt gca tca gca atg act tgg ata gca agg aca aga gct	817
Ser Phe Glu Val Ala Ser Ala Met Thr Trp Ile Ala Arg Thr Arg Ala	
255 260 265	
ttt caa att cca gaa agt gag tac gtg aaa att ctc ttc gga atg gac	865
Phe Gln Ile Pro Glu Ser Glu Tyr Val Lys Ile Leu Phe Gly Met Asp	
270 275 280 285	
atg agg aac tca ttt aat ccc cct ctt cca agc gga tac tat ggt aac	913
Met Arg Asn Ser Phe Asn Pro Pro Leu Pro Ser Gly Tyr Tyr Gly Asn	
290 295 300	

tcc att ggt acc gca tgt gca gtg gat aat gtt caa gac ctc tta agt	961
Ser Ile Gly Thr Ala Cys Ala Val Asp Asn Val Gln Asp Leu Leu Ser	
305 310 315	
gga tct ctt ttg cgt gct ata atg att ata aag aaa tca aag gtc tct	1009
Gly Ser Leu Leu Arg Ala Ile Met Ile Ile Lys Lys Ser Lys Val Ser	
320 325 330	
tta aat gat aat ttc aag tca aga gct gtg gtg aag cca tct gaa ttg	1057
Leu Asn Asp Asn Phe Lys Ser Arg Ala Val Val Lys Pro Ser Glu Leu	
335 340 345	
gat gtg aat atg aat cat gaa aac gta gtt gca ttt gct gat tgg agc	1105
Asp Val Asn Met Asn His Glu Asn Val Val Ala Phe Ala Asp Trp Ser	
350 355 360 365	
cga ttg gga ttt gat gaa gtg gat ttt ggt tgg ggg aat gcg gtg agt	1153
Arg Leu Gly Phe Asp Glu Val Asp Phe Gly Trp Gly Asn Ala Val Ser	
370 375 380	
gta agc cct gtg caa caa cag tct gcg tta gca atg caa aat tat ttt	1201
Val Ser Pro Val Gln Gln Gln Ser Ala Leu Ala Met Gln Asn Tyr Phe	
385 390 395	
ctt ttc cta aaa cct tcc aag aac aag ccc gat gga atc aaa ata tta	1249
Leu Phe Leu Lys Pro Ser Lys Asn Lys Pro Asp Gly Ile Lys Ile Leu	
400 405 410	
atg ttt ctg ccc cta tca aaa atg aag tca ttc aaa att gaa atg gaa	1297
Met Phe Leu Pro Leu Ser Lys Met Lys Ser Phe Lys Ile Glu Met Glu	
415 420 425	
gcc atg atg aaa aaa tat gtg gct aaa gta tga aagtgcaacg atggaaggct	1350
Ala Met Met Lys Lys Tyr Val Ala Lys Val	
430 435	
tgtatttttg aaataatatt tcaaataatc tcgtggttca aataactttgt taataaaaaaa	1410
aaaaaaaaa	1419
<210> 22	
<211> 439	
<212> PRT	
<213> Taxus cuspidata	
<400> 22	
Met Glu Lys Thr Asp Leu His Val Asn Leu Ile Glu Lys Val Met Val	
1 5 10 15	
Gly Pro Ser Pro Pro Leu Pro Lys Thr Thr Leu Gln Leu Ser Ser Ile	
20 25 30	
Asp Asn Leu Pro Gly Val Arg Gly Ser Ile Phe Asn Ala Leu Leu Ile	
35 40 45	
Tyr Asn Ala Ser Pro Ser Pro Thr Met Ile Ser Ala Asp Pro Ala Lys	

50	55	60
Pro Ile Arg Glu Ala Leu Ala Lys Ile Leu Val Tyr Tyr Pro Pro Phe 65 70 75 80		
Ala Gly Arg Leu Arg Glu Thr Glu Asn Gly Asp Leu Glu Val Glu Cys 85 90 95		
Thr Gly Glu Gly Ala Met Phe Leu Glu Ala Met Ala Asp Asn Glu Leu 100 105 110		
Ser Val Leu Gly Asp Phe Asp Asp Ser Asn Pro Ser Phe Gln Gln Leu 115 120 125		
Leu Phe Ser Leu Pro Leu Asp Thr Asn Phe Lys Asp Leu Ser Leu Leu 130 135 140		
Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val 145 150 155 160		
Ser Phe His His Gly Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Leu 165 170 175		
Lys Gly Leu Ala Glu Met Ala Arg Gly Glu Val Lys Leu Ser Leu Glu 180 185 190		
Pro Ile Trp Asn Arg Glu Leu Val Lys Leu Asp Asp Pro Lys Tyr Leu 195 200 205		
Gln Phe Phe His Phe Glu Phe Leu Arg Ala Pro Ser Ile Val Glu Lys 210 215 220		
Ile Val Gln Thr Tyr Phe Ile Ile Asp Phe Glu Thr Ile Asn Tyr Ile 225 230 235 240		
Lys Gln Ser Val Met Glu Glu Cys Lys Glu Phe Cys Ser Ser Phe Glu 245 250 255		
Val Ala Ser Ala Met Thr Trp Ile Ala Arg Thr Arg Ala Phe Gln Ile 260 265 270		
Pro Glu Ser Glu Tyr Val Lys Ile Leu Phe Gly Met Asp Met Arg Asn 275 280 285		
Ser Phe Asn Pro Pro Leu Pro Ser Gly Tyr Tyr Gly Asn Ser Ile Gly 290 295 300		

Thr Ala Cys Ala Val Asp Asn Val Gln Asp Leu Leu Ser Gly Ser Leu
305 310 315 320

Leu Arg Ala Ile Met Ile Ile Lys Lys Ser Lys Val Ser Leu Asn Asp
325 330 335

Asn Phe Lys Ser Arg Ala Val Val Lys Pro Ser Glu Leu Asp Val Asn
340 345 350

Met Asn His Glu Asn Val Val Ala Phe Ala Asp Trp Ser Arg Leu Gly
355 360 365

Phe Asp Glu Val Asp Phe Gly Trp Gly Asn Ala Val Ser Val Ser Pro
370 375 380

Val Gln Gln Gln Ser Ala Leu Ala Met Gln Asn Tyr Phe Leu Phe Leu
385 390 395 400

Lys Pro Ser Lys Asn Lys Pro Asp Gly Ile Lys Ile Leu Met Phe Leu
405 410 415

Pro Leu Ser Lys Met Lys Ser Phe Lys Ile Glu Met Glu Ala Met Met
420 425 430

Lys Lys Tyr Val Ala Lys Val
435

<210> 23
<211> 1388
<212> DNA
<213> Taxus cuspidata

<220>
<221> CDS
<222> (22)..(1344)
<223> coding sequence

<400> 23
aggagagtcc aaatatctac a atg ggc agg ttc aat gta gat atg att gag 51
Met Gly Arg Phe Asn Val Asp Met Ile Glu
1 5 10

cga gtg atc gtg gcg cca tgc ctt caa tcg ccc aaa aat atc ctg cac 99
Arg Val Ile Val Ala Pro Cys Leu Gln Ser Pro Lys Asn Ile Leu His
15 20 25

ctc tcc ccc att gac aac aaa act aga gga cta acc aac ata tta tca 147
Leu Ser Pro Ile Asp Asn Lys Thr Arg Gly Leu Thr Asn Ile Leu Ser
30 35 40

gtc tac aat gcc tcc cag aga gtt tct gtt tct gca gat cct gca aaa	195
Val Tyr Asn Ala Ser Gln Arg Val Ser Val Ser Ala Asp Pro Ala Lys	
45 50 55	
aca att cga gag gct ctc tcc aag gtg ctg gtt tat tat ccc cct ttt	243
Thr Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Pro Pro Phe	
60 65 70	
gct gga agg ctg aga aac aca gaa aat ggg gat ctt gaa gtg gag tgc	291
Ala Gly Arg Leu Arg Asn Thr Glu Asn Gly Asp Leu Glu Val Glu Cys	
75 80 85 90	
aca ggg gag ggt gcc gtc ttt gtg gaa gcc atg gcg gac aac gac ctt	339
Thr Gly Glu Gly Ala Val Phe Val Glu Ala Met Ala Asp Asn Asp Leu	
95 100 105	
tca gta tta caa gat ttc aat gag tac gat cca tca ttt cag cag cta	387
Ser Val Leu Gln Asp Phe Asn Glu Tyr Asp Pro Ser Phe Gln Gln Leu	
110 115 120	
gtt ttt aat ctt cga gag gat gtc aat att gag gac ctc cat ctt cta	435
Val Phe Asn Leu Arg Glu Asp Val Asn Ile Glu Asp Leu His Leu Leu	
125 130 135	
act gtt cag gta act cgt ttt aca tgt gga gga ttt gtt gtg ggc aca	483
Thr Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Thr	
140 145 150	
aga ttc cac cat agt gta tct gat gga aaa gga atc ggc cag tta ctt	531
Arg Phe His His Ser Val Ser Asp Gly Lys Gly Ile Gly Gln Leu Leu	
155 160 165 170	
aaa ggc atg gga gag atg gca agg ggg gag ttt aag ccc tcg tta gaa	579
Lys Gly Met Gly Glu Met Ala Arg Gly Glu Phe Lys Pro Ser Leu Glu	
175 180 185	
cca ata tgg aat aga gaa atg gtg aag cct gaa gac att atg tac ctc	627
Pro Ile Trp Asn Arg Glu Met Val Lys Pro Glu Asp Ile Met Tyr Leu	
190 195 200	
cag ttt gat cac ttt gat ttc ata cac cca cct ctt aat ctt gag aag	675
Gln Phe Asp His Phe Asp Phe Ile His Pro Pro Leu Asn Leu Glu Lys	
205 210 215	
tct att caa gca tct atg gta ata agc ttt gag aga ata aat tat atc	723
Ser Ile Gln Ala Ser Met Val Ile Ser Phe Glu Arg Ile Asn Tyr Ile	
220 225 230	
aaa cga tgc atg atg gaa gaa tgc aaa gaa ttt ttt tct gca ttt gaa	771
Lys Arg Cys Met Met Glu Glu Cys Lys Glu Phe Phe Ser Ala Phe Glu	
235 240 245 250	
gtt gta gta gca ttg att tgg ctg gca agg aca aag tct ttt cga att	819
Val Val Val Ala Leu Ile Trp Leu Ala Arg Thr Lys Ser Phe Arg Ile	
255 260 265	
cca ccc aat gag tat gtg aaa att atc ttt cca atc gac atg agg aat	867
Pro Pro Asn Glu Tyr Val Lys Ile Ile Phe Pro Ile Asp Met Arg Asn	
270 275 280	

tca ttt gac tcc cct ctt cca aag gga tac tat ggt aat gct att ggt	915
Ser Phe Asp Ser Pro Leu Pro Lys Gly Tyr Tyr Gly Asn Ala Ile Gly	
285 290 295	
aat gca tgt gca atg gat aat gtc aaa gac ctc tta aat gga tct ctt	963
Asn Ala Cys Ala Met Asp Asn Val Lys Asp Leu Leu Asn Gly Ser Leu	
300 305 310	
tta tat gct cta atg ctt ata aag aaa tca aag ttt gct tta aat gag	1011
Leu Tyr Ala Leu Met Leu Ile Lys Lys Ser Lys Phe Ala Leu Asn Glu	
315 320 325 330	
aat ttc aaa tca aga atc ttg aca aaa cca tct aca tta gat gcg aat	1059
Asn Phe Lys Ser Arg Ile Leu Thr Lys Pro Ser Thr Leu Asp Ala Asn	
335 340 345	
atg aag cat gaa aat gta gtc gga tgt ggc gat tgg agg aat ttg gga	1107
Met Lys His Glu Asn Val Val Gly Cys Gly Asp Trp Arg Asn Leu Gly	
350 355 360	
ttt tat gaa gca gat ttt gga tgg gga aat gca gtg aat gta agc ccc	1155
Phe Tyr Glu Ala Asp Phe Gly Trp Gly Asn Ala Val Asn Val Ser Pro	
365 370 375	
atg cag caa caa aga gag cat gaa tta gct atg caa aat tat ttt ctt	1203
Met Gln Gln Gln Arg Glu His Glu Leu Ala Met Gln Asn Tyr Phe Leu	
380 385 390	
ttt ctc cga tca gct aag aac atg att gat gga atc aag ata cta atg	1251
Phe Leu Arg Ser Ala Lys Asn Met Ile Asp Gly Ile Lys Ile Leu Met	
395 400 405 410	
ttc atg cct gca tca atg gtg aaa cca ttc aaa att gaa atg gaa gtc	1299
Phe Met Pro Ala Ser Met Val Lys Pro Phe Lys Ile Glu Met Glu Val	
415 420 425	
aca ata aac aaa tat gtg gct aaa ata tgt aac tct aag tta taa	1344
Thr Ile Asn Lys Tyr Val Ala Lys Ile Cys Asn Ser Lys Leu	
430 435 440	
agtatgtatg actgcaaaat agtaaaatat tgcattggtgg atgc	1388

<210> 24
 <211> 440
 <212> PRT
 <213> Taxus cuspidata

<400> 24

Met Gly Arg Phe Asn Val Asp Met Ile Glu Arg Val Ile Val Ala Pro
1 5 10 15

Cys Leu Gln Ser Pro Lys Asn Ile Leu His Leu Ser Pro Ile Asp Asn
20 25 30

Lys Thr Arg Gly Leu Thr Asn Ile Leu Ser Val Tyr Asn Ala Ser Gln
35 40 45

Arg Val Ser Val Ser Ala Asp Pro Ala Lys Thr Ile Arg Glu Ala Leu
 50 55 60

Ser Lys Val Leu Val Tyr Tyr Pro Pro Phe Ala Gly Arg Leu Arg Asn
 65 70 75 80

Thr Glu Asn Gly Asp Leu Glu Val Glu Cys Thr Gly Glu Gly Ala Val
 85 90 95

Phe Val Glu Ala Met Ala Asp Asn Asp Leu Ser Val Leu Gln Asp Phe
 100 105 110

Asn Glu Tyr Asp Pro Ser Phe Gln Gln Leu Val Phe Asn Leu Arg Glu
 115 120 125

Asp Val Asn Ile Glu Asp Leu His Leu Leu Thr Val Gln Val Thr Arg
 130 135 140

Phe Thr Cys Gly Gly Phe Val Val Gly Thr Arg Phe His His Ser Val
 145 150 155 160

Ser Asp Gly Lys Gly Ile Gly Gln Leu Leu Lys Gly Met Gly Glu Met
 165 170 175

Ala Arg Gly Glu Phe Lys Pro Ser Leu Glu Pro Ile Trp Asn Arg Glu
 180 185 190

Met Val Lys Pro Glu Asp Ile Met Tyr Leu Gln Phe Asp His Phe Asp
 195 200 205

Phe Ile His Pro Pro Leu Asn Leu Glu Lys Ser Ile Gln Ala Ser Met
 210 215 220

Val Ile Ser Phe Glu Arg Ile Asn Tyr Ile Lys Arg Cys Met Met Glu
 225 230 235 240

Glu Cys Lys Glu Phe Phe Ser Ala Phe Glu Val Val Val Ala Leu Ile
 245 250 255

Trp Leu Ala Arg Thr Lys Ser Phe Arg Ile Pro Pro Asn Glu Tyr Val
 260 265 270

Lys Ile Ile Phe Pro Ile Asp Met Arg Asn Ser Phe Asp Ser Pro Leu
 275 280 285

Pro Lys Gly Tyr Tyr Gly Asn Ala Ile Gly Asn Ala Cys Ala Met Asp
 290 295 300

Asn Val Lys Asp Leu Leu Asn Gly Ser Leu Leu Tyr Ala Leu Met Leu
 305 310 315 320

Ile Lys Lys Ser Lys Phe Ala Leu Asn Glu Asn Phe Lys Ser Arg Ile
 325 330 335

Leu Thr Lys Pro Ser Thr Leu Asp Ala Asn Met Lys His Glu Asn Val
 340 345 350

Val Gly Cys Gly Asp Trp Arg Asn Leu Gly Phe Tyr Glu Ala Asp Phe
 355 360 365

Gly Trp Gly Asn Ala Val Asn Val Ser Pro Met Gln Gln Gln Arg Glu
 370 375 380

His Glu Leu Ala Met Gln Asn Tyr Phe Leu Phe Leu Arg Ser Ala Lys
 385 390 395 400

Asn Met Ile Asp Gly Ile Lys Ile Leu Met Phe Met Pro Ala Ser Met
 405 410 415

Val Lys Pro Phe Lys Ile Glu Met Glu Val Thr Ile Asn Lys Tyr Val
 420 425 430

Ala Lys Ile Cys Asn Ser Lys Leu
 435 440

<210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> modified_base
 <222> (6)..(6)
 <223> I

<220>
 <221> modified_base
 <222> (9)..(9)
 <223> I

<220>
 <221> modified_base

<222> (14)..(14)
<223> I

<400> 25
ttymgncna gmgnttygar

20

<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> modified_base
<222> (6)..(6)
<223> I

<220>
<221> modified_base
<222> (9)..(9)
<223> I

<220>
<221> modified_base
<222> (12)..(12)
<223> I

<220>
<221> modified_base
<222> (15)..(15)
<223> I

<400> 26
ttymgncnt cnmgnttyga r

21

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> modified_base
<222> (3)..(6)
<223> I

<220>
<221> modified_base
<222> (9)..(9)
<223> I

<220>
<221> modified_base

<222> (12)..(12)
 <223> I

 <220>
 <221> modified_base
 <222> (18)..(18)
 <223> I

 <400> 27
 cknennccng cncraangg 20

 <210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <220>
 <221> modified_base
 <222> (12)..(12)
 <223> I

 <220>
 <221> modified_base
 <222> (15)..(15)
 <223> I

 <400> 28
 gargarttym gnccngarmg 20

 <210> 29
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <220>
 <221> modified_base
 <222> (10)..(12)
 <223> I

 <220>
 <221> modified_base
 <222> (15)..(15)
 <223> I

 <220>
 <221> modified_base
 <222> (18)..(18)
 <223> I

 <400> 29
 garaarttyn nnccnganar gtty 24

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> modified_base
<222> (6)..(9)
<223> I

<220>
<221> modified_base
<222> (12)..(15)
<223> I

<220>
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<222> (18)..(18)
<223> I

<220>
<221> modified_base
<222> (21)..(21)
<223> I

<220>
<221> modified_base
<222> (27)..(27)
<223> I

<400> 30
ggrcannnnc knnnnccncc nccraangg

29

<210> 31
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> modified_base
<222> (3)..(3)
<223> I

<220>
<221> modified_base
<222> (9)..(9)
<223> I

<220>
<221> modified_base

<222> (12)..(12)
 <223> I

 <220>
 <221> modified_base
 <222> (18)..(18)
 <223> I

 <220>
 <221> modified_base
 <222> (21)..(21)
 <223> I

 <220>
 <221> modified_base
 <222> (24)..(24)
 <223> I

 <220>
 <221> modified_base
 <222> (30)..(30)
 <223> I

 <400> 31
 ccnggrcana tnmkyytncc ngcnccraan gg 32

 <210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 32
 atggacgccc tgtataagag 20

 <210> 33
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 33
 tcaattgact atggtctcgg 20

 <210> 34
 <211> 1488
 <212> DNA
 <213> Taxus cuspidata

 <220>
 <221> CDS
 <222> (24)..(1346)
 <223> coding sequence

<400> 34

gcaccagctg agcttgatct gag atg gca ggc tca aca gaa ttt gtg gta aga	53
Met Ala Gly Ser Thr Glu Phe Val Val Arg	
1 5 10	
agc tta gag aga gtg atg gtg gct cca agc cag cca tcg ccc aaa gct	101
Ser Leu Glu Arg Val Met Val Ala Pro Ser Gln Pro Ser Pro Lys Ala	
15 20 25	
ttc ctg cag ctc tcc acc ctt gac aat cta cca ggg gtg aga gaa aac	149
Phe Leu Gln Leu Ser Thr Leu Asp Asn Leu Pro Gly Val Arg Glu Asn	
30 35 40	
att ttt aac acc ttg tta gtc tac aat gcc tca gac aga gtt tcc gta	197
Ile Phe Asn Thr Leu Leu Val Tyr Asn Ala Ser Asp Arg Val Ser Val	
45 50 55	
gat cct gca aaa gta att cgg cag gct ctc tcc aag gtg ttg gtg tac	245
Asp Pro Ala Lys Val Ile Arg Gln Ala Leu Ser Lys Val Leu Val Tyr	
60 65 70	
tat tcc cct ttt gca ggg cgt ctc agg aaa aaa gaa aat gga gat ctt	293
Tyr Ser Pro Phe Ala Gly Arg Leu Arg Lys Lys Glu Asn Gly Asp Leu	
75 80 85 90	
gaa gtg gag tgc aca ggg gag ggt gct ctg ttt gtg gaa gcc atg gct	341
Glu Val Glu Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala Met Ala	
95 100 105	
gac act gac ctc tca gtc tta gga gat ttg gat gac tac agt cct tca	389
Asp Thr Asp Leu Ser Val Leu Gly Asp Leu Asp Asp Tyr Ser Pro Ser	
110 115 120	
ctt gag caa cta ctt ttt tgt ctt ccg cct gat aca gat att gag gac	437
Leu Glu Gln Leu Leu Phe Cys Leu Pro Pro Asp Thr Asp Ile Glu Asp	
125 130 135	
atc cat cct ctg gtg gtt cag gta act cgt ttt aca tgt gga ggt ttt	485
Ile His Pro Leu Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe	
140 145 150	
gtt gta ggg gtg agt ttc tgc cat ggt ata tgt gat gga cta gga gca	533
Val Val Gly Val Ser Phe Cys His Gly Ile Cys Asp Gly Leu Gly Ala	
155 160 165 170	
ggc cag ttt ctt ata gcc atg gga gag atg gca agg gga gag att aag	581
Gly Gln Phe Leu Ile Ala Met Gly Glu Met Ala Arg Gly Glu Ile Lys	
175 180 185	
ccc tcc tcg gag cca ata tgg aag aga gaa ttg ctg aag ccg gaa gac	629
Pro Ser Ser Glu Pro Ile Trp Lys Arg Glu Leu Leu Lys Pro Glu Asp	
190 195 200	
cct tta tac cgg ttc cag tat tat cac ttt caa ttg att tgc ccg cct	677
Pro Leu Tyr Arg Phe Gln Tyr Tyr His Phe Gln Leu Ile Cys Pro Pro	
205 210 215	
tca aca ttc ggg aaa ata gtt caa gga tct ctt gtt ata acc tct gag	725
Ser Thr Phe Gly Lys Ile Val Gln Gly Ser Leu Val Ile Thr Ser Glu	
220 225 230	

aca ata aat tgt atc aaa caa tgc ctt agg gaa gaa agt aaa gaa ttt	773
Thr Ile Asn Cys Ile Lys Gln Cys Leu Arg Glu Glu Ser Lys Glu Phe	
235 240 245 250	
tgc tct gcg ttc gaa gtt gta tct gca ttg gct tgg ata gca agg aca	821
Cys Ser Ala Phe Glu Val Val Ser Ala Leu Ala Trp Ile Ala Arg Thr	
255 260 265	
agg gct ctt caa att cca cat agt gag aat gtg aag ctt att ttt gca	869
Arg Ala Leu Gln Ile Pro His Ser Glu Asn Val Lys Leu Ile Phe Ala	
270 275 280	
atg gac atg aga aaa tta ttt aat cca cca ctt tcg aag gga tac tac	917
Met Asp Met Arg Lys Leu Phe Asn Pro Pro Leu Ser Lys Gly Tyr Tyr	
285 290 295	
ggg aat ttt gtt ggt acc gta tgt gca atg gat aat gtc aag gac cta	965
Gly Asn Phe Val Gly Thr Val Cys Ala Met Asp Asn Val Lys Asp Leu	
300 305 310	
tta agt gga tct ctt ttg cgt gtt gta agg att ata aag aaa gca aag	1013
Leu Ser Gly Ser Leu Leu Arg Val Val Arg Ile Ile Lys Lys Ala Lys	
315 320 325 330	
gtc tct tta aat gag cat ttc acg tca aca atc gtg aca ccc cgt tct	1061
Val Ser Leu Asn Glu His Phe Thr Ser Thr Ile Val Thr Pro Arg Ser	
335 340 345	
gga tca gat gag agt atc aat tat gaa aac ata gtt gga ttt ggt gat	1109
Gly Ser Asp Glu Ser Ile Asn Tyr Glu Asn Ile Val Gly Phe Gly Asp	
350 355 360	
cga agg cga ttg gga ttt gat gaa gta gac ttt ggg tgg ggg cat gca	1157
Arg Arg Arg Leu Gly Phe Asp Glu Val Asp Phe Gly Trp Gly His Ala	
365 370 375	
gat aat gta agt ctc gtg caa cat gga ttg aag gat gtt tca gtc gtg	1205
Asp Asn Val Ser Leu Val Gln His Gly Leu Lys Asp Val Ser Val Val	
380 385 390	
caa agt tat ttt ctt ttc ata cga cct ccc aag aat aac ccc gat gga	1253
Gln Ser Tyr Phe Leu Phe Ile Arg Pro Pro Lys Asn Asn Pro Asp Gly	
395 400 405 410	
atc aag atc cta tcg ttc atg ccc ccg tca ata gtg aaa tcc ttc aaa	1301
Ile Lys Ile Leu Ser Phe Met Pro Pro Ser Ile Val Lys Ser Phe Lys	
415 420 425	
ttt gaa atg gaa acc atg aca aac aaa tat gta act aag cct tga	1346
Phe Glu Met Glu Thr Met Thr Asn Lys Tyr Val Thr Lys Pro	
430 435 440	
aattgtagta acttaagcct tgcattttca gaataagttt tggcactggg ttgtggttga	1406
agtaatgtac ttttgaattt tgatttaaag ttctattcaa agttataaaa tgtattatgt	1466
gaaaatatgt tgcaattatg gt	1488

<210> 35

<211> 440
 <212> PRT
 <213> Taxus cuspidata

<400> 35

Met Ala Gly Ser Thr Glu Phe Val Val Arg Ser Leu Glu Arg Val Met
 1 5 10 15

Val Ala Pro Ser Gln Pro Ser Pro Lys Ala Phe Leu Gln Leu Ser Thr
 20 25 30

Leu Asp Asn Leu Pro Gly Val Arg Glu Asn Ile Phe Asn Thr Leu Leu
 35 40 45

Val Tyr Asn Ala Ser Asp Arg Val Ser Val Asp Pro Ala Lys Val Ile
 50 55 60

Arg Gln Ala Leu Ser Lys Val Leu Val Tyr Tyr Ser Pro Phe Ala Gly
 65 70 75 80

Arg Leu Arg Lys Lys Glu Asn Gly Asp Leu Glu Val Glu Cys Thr Gly
 85 90 95

Glu Gly Ala Leu Phe Val Glu Ala Met Ala Asp Thr Asp Leu Ser Val
 100 105 110

Leu Gly Asp Leu Asp Asp Tyr Ser Pro Ser Leu Glu Gln Leu Leu Phe
 115 120 125

Cys Leu Pro Pro Asp Thr Asp Ile Glu Asp Ile His Pro Leu Val Val
 130 135 140

Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val Ser Phe
 145 150 155 160

Cys His Gly Ile Cys Asp Gly Leu Gly Ala Gly Gln Phe Leu Ile Ala
 165 170 175

Met Gly Glu Met Ala Arg Gly Glu Ile Lys Pro Ser Ser Glu Pro Ile
 180 185 190

Trp Lys Arg Glu Leu Leu Lys Pro Glu Asp Pro Leu Tyr Arg Phe Gln
 195 200 205

Tyr Tyr His Phe Gln Leu Ile Cys Pro Pro Ser Thr Phe Gly Lys Ile
 210 215 220

Val Gln Gly Ser Leu Val Ile Thr Ser Glu Thr Ile Asn Cys Ile Lys
 225 230 235 240

Gln Cys Leu Arg Glu Glu Ser Lys Glu Phe Cys Ser Ala Phe Glu Val
 245 250 255

Val Ser Ala Leu Ala Trp Ile Ala Arg Thr Arg Ala Leu Gln Ile Pro
 260 265 270

His Ser Glu Asn Val Lys Leu Ile Phe Ala Met Asp Met Arg Lys Leu
 275 280 285

Phe Asn Pro Pro Leu Ser Lys Gly Tyr Tyr Gly Asn Phe Val Gly Thr
 290 295 300

Val Cys Ala Met Asp Asn Val Lys Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320

Arg Val Val Arg Ile Ile Lys Lys Ala Lys Val Ser Leu Asn Glu His
 325 330 335

Phe Thr Ser Thr Ile Val Thr Pro Arg Ser Gly Ser Asp Glu Ser Ile
 340 345 350

Asn Tyr Glu Asn Ile Val Gly Phe Gly Asp Arg Arg Arg Leu Gly Phe
 355 360 365

Asp Glu Val Asp Phe Gly Trp Gly His Ala Asp Asn Val Ser Leu Val
 370 375 380

Gln His Gly Leu Lys Asp Val Ser Val Val Gln Ser Tyr Phe Leu Phe
 385 390 395 400

Ile Arg Pro Pro Lys Asn Asn Pro Asp Gly Ile Lys Ile Leu Ser Phe
 405 410 415

Met Pro Pro Ser Ile Val Lys Ser Phe Lys Phe Glu Met Glu Thr Met
 420 425 430

Thr Asn Lys Tyr Val Thr Lys Pro
 435 440

<210> 36
 <211> 1338
 <212> DNA
 <213> Taxus cuspidata


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<220>
<221> CDS
<222> (1)..(1326)
<223> coding sequence

<400> 36
atg aag aag aca ggt tcg ttt gca gag ttc cat gtg aat atg att gag      48
Met Lys Lys Thr Gly Ser Phe Ala Glu Phe His Val Asn Met Ile Glu
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cga gtc atg gtg aga ccg tgc ctg cct tcg ccc aaa aca atc ctc cct      96
Arg Val Met Val Arg Pro Cys Leu Pro Ser Pro Lys Thr Ile Leu Pro
          20          25          30

ctc tcc gcc att gac aac atg gca aga gct ttt tct aac gta ttg ctg      144
Leu Ser Ala Ile Asp Asn Met Ala Arg Ala Phe Ser Asn Val Leu Leu
          35          40          45

gtc tac gct gcc aac atg gac aga gtc tct gca gat cct gca aaa gtg      192
Val Tyr Ala Ala Asn Met Asp Arg Val Ser Ala Asp Pro Ala Lys Val
          50          55          60

att cga gag gct ctc tcc aag gtg ctg gtt tat tat tac cct ttt gct      240
Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Tyr Pro Phe Ala
65          70          75          80

ggg cgg ctc aga aat aaa gaa aat ggg gaa ctt gaa gtg gag tgc aca      288
Gly Arg Leu Arg Asn Lys Glu Asn Gly Glu Leu Glu Val Glu Cys Thr
          85          90          95

ggg cag ggt gtt ctg ttt ctg gaa gcc atg gct gac agc gac ctt tca      336
Gly Gln Gly Val Leu Phe Leu Glu Ala Met Ala Asp Ser Asp Leu Ser
          100          105          110

gtc tta aca gat ctg gat aac tac aat cca tcg ttt cag cag ttg att      384
Val Leu Thr Asp Leu Asp Asn Tyr Asn Pro Ser Phe Gln Gln Leu Ile
          115          120          125

ttt tct cta cca cag gat aca gat att gag gac ctc cat ctc ttg att      432
Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp Leu His Leu Leu Ile
          130          135          140

gtt cag gta act cgt ttt aca tgt ggg ggt ttt gtt gtg gga gcg aat      480
Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Ala Asn
145          150          155          160

gtg tat ggt agt gca tgc gat gca aaa gga ttt ggc cag ttt ctt caa      528
Val Tyr Gly Ser Ala Cys Asp Ala Lys Gly Phe Gly Gln Phe Leu Gln
          165          170          175

agt atg gca gag atg gcg aga gga gag gtt aag ccc tcg att gaa ccg      576
Ser Met Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Ile Glu Pro
          180          185          190

ata tgg aat aga gaa ctg gtg aag cta gaa cat tgt atg ccc ttc cgg      624
Ile Trp Asn Arg Glu Leu Val Lys Leu Glu His Cys Met Pro Phe Arg
          195          200          205

atg agt cat ctt caa att ata cat gca cct gta att gag gag aaa ttt      672

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Met	Ser	His	Leu	Gln	Ile	Ile	His	Ala	Pro	Val	Ile	Glu	Glu	Lys	Phe	
210						215					220					
gtt	caa	aca	tct	ctt	gtt	ata	aac	ttt	gag	ata	ata	aat	cat	atc	aga	720
Val	Gln	Thr	Ser	Leu	Val	Ile	Asn	Phe	Glu	Ile	Ile	Asn	His	Ile	Arg	
225					230				235						240	
cga	cgc	atc	atg	gaa	gaa	cgc	aaa	gaa	agt	tta	tct	tca	ttt	gaa	att	768
Arg	Arg	Ile	Met	Glu	Glu	Arg	Lys	Glu	Ser	Leu	Ser	Ser	Phe	Glu	Ile	
				245				250						255		
gta	gca	gca	ttg	gtt	tgg	cta	gca	aag	ata	aag	gct	ttt	caa	att	cca	816
Val	Ala	Ala	Leu	Val	Trp	Leu	Ala	Lys	Ile	Lys	Ala	Phe	Gln	Ile	Pro	
			260				265						270			
cat	agt	gag	aat	gtg	aag	ctt	ctt	ttt	gca	atg	gac	ttg	agg	aga	tca	864
His	Ser	Glu	Asn	Val	Lys	Leu	Leu	Phe	Ala	Met	Asp	Leu	Arg	Arg	Ser	
		275				280						285				
ttt	aat	ccc	cct	ctt	cca	cat	gga	tac	tat	ggc	aat	gcc	ttt	ggg	att	912
Phe	Asn	Pro	Pro	Leu	Pro	His	Gly	Tyr	Tyr	Gly	Asn	Ala	Phe	Gly	Ile	
	290					295				300						
gca	tgt	gca	atg	gat	aat	gtc	cat	gac	ctt	cta	agt	gga	tct	ctt	ttg	960
Ala	Cys	Ala	Met	Asp	Asn	Val	His	Asp	Leu	Leu	Ser	Gly	Ser	Leu	Leu	
305					310				315						320	
cgc	act	ata	atg	atc	ata	aag	aaa	tca	aag	ttc	tct	tta	cac	aaa	gaa	1008
Arg	Thr	Ile	Met	Ile	Ile	Lys	Lys	Ser	Lys	Phe	Ser	Leu	His	Lys	Glu	
				325				330						335		
ctc	aac	tca	aaa	acc	gtg	atg	agc	tca	tct	gta	gta	gat	gtc	aat	acg	1056
Leu	Asn	Ser	Lys	Thr	Val	Met	Ser	Ser	Ser	Val	Val	Asp	Val	Asn	Thr	
			340					345					350			
aag	ttt	gaa	gat	gta	gtt	tca	att	agt	gat	tgg	agg	cat	tct	ata	tat	1104
Lys	Phe	Glu	Asp	Val	Val	Ser	Ile	Ser	Asp	Trp	Arg	His	Ser	Ile	Tyr	
		355				360						365				
tat	gaa	gtg	gac	ttt	ggg	tgg	gga	gat	gca	atg	aac	gtg	agc	act	atg	1152
Tyr	Glu	Val	Asp	Phe	Gly	Trp	Gly	Asp	Ala	Met	Asn	Val	Ser	Thr	Met	
	370				375						380					
cta	caa	caa	cag	gag	cac	gag	aaa	tct	ctg	cca	act	tat	ttt	tct	ttc	1200
Leu	Gln	Gln	Gln	Glu	His	Glu	Lys	Ser	Leu	Pro	Thr	Tyr	Phe	Ser	Phe	
385					390				395						400	
cta	caa	tct	act	aag	aac	atg	cca	gat	gga	atc	aag	atg	cta	atg	ttt	1248
Leu	Gln	Ser	Thr	Lys	Asn	Met	Pro	Asp	Gly	Ile	Lys	Met	Leu	Met	Phe	
				405				410					415			
atg	cct	cca	tca	aaa	ctg	aaa	aaa	ttc	aaa	att	gaa	ata	gaa	gct	atg	1296
Met	Pro	Pro	Ser	Lys	Leu	Lys	Lys	Phe	Lys	Ile	Glu	Ile	Glu	Ala	Met	
			420					425					430			
ata	aaa	aaa	tat	gtg	act	aaa	gtg	tgt	ccg	tcaa	agttat	ga				1338
Ile	Lys	Lys	Tyr	Val	Thr	Lys	Val	Cys	Pro							
		435					440									

<210> 37

<211> 442
 <212> PRT
 <213> Taxus cuspidata

<400> 37

Met Lys Lys Thr Gly Ser Phe Ala Glu Phe His Val Asn Met Ile Glu
 1 5 10 15

Arg Val Met Val Arg Pro Cys Leu Pro Ser Pro Lys Thr Ile Leu Pro
 20 25 30

Leu Ser Ala Ile Asp Asn Met Ala Arg Ala Phe Ser Asn Val Leu Leu
 35 40 45

Val Tyr Ala Ala Asn Met Asp Arg Val Ser Ala Asp Pro Ala Lys Val
 50 55 60

Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Tyr Pro Phe Ala
 65 70 75 80

Gly Arg Leu Arg Asn Lys Glu Asn Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95

Gly Gln Gly Val Leu Phe Leu Glu Ala Met Ala Asp Ser Asp Leu Ser
 100 105 110

Val Leu Thr Asp Leu Asp Asn Tyr Asn Pro Ser Phe Gln Gln Leu Ile
 115 120 125

Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp Leu His Leu Leu Ile
 130 135 140

Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Ala Asn
 145 150 155 160

Val Tyr Gly Ser Ala Cys Asp Ala Lys Gly Phe Gly Gln Phe Leu Gln
 165 170 175

Ser Met Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Ile Glu Pro
 180 185 190

Ile Trp Asn Arg Glu Leu Val Lys Leu Glu His Cys Met Pro Phe Arg
 195 200 205

Met Ser His Leu Gln Ile Ile His Ala Pro Val Ile Glu Glu Lys Phe
 210 215 220

Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile Ile Asn His Ile Arg
 225 230 235 240

Arg Arg Ile Met Glu Glu Arg Lys Glu Ser Leu Ser Ser Phe Glu Ile
 245 250 255

Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys Ala Phe Gln Ile Pro
 260 265 270

His Ser Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Arg Ser
 275 280 285

Phe Asn Pro Pro Leu Pro His Gly Tyr Tyr Gly Asn Ala Phe Gly Ile
 290 295 300

Ala Cys Ala Met Asp Asn Val His Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320

Arg Thr Ile Met Ile Ile Lys Lys Ser Lys Phe Ser Leu His Lys Glu
 325 330 335

Leu Asn Ser Lys Thr Val Met Ser Ser Ser Val Val Asp Val Asn Thr
 340 345 350

Lys Phe Glu Asp Val Val Ser Ile Ser Asp Trp Arg His Ser Ile Tyr
 355 360 365

Tyr Glu Val Asp Phe Gly Trp Gly Asp Ala Met Asn Val Ser Thr Met
 370 375 380

Leu Gln Gln Gln Glu His Glu Lys Ser Leu Pro Thr Tyr Phe Ser Phe
 385 390 395 400

Leu Gln Ser Thr Lys Asn Met Pro Asp Gly Ile Lys Met Leu Met Phe
 405 410 415

Met Pro Pro Ser Lys Leu Lys Lys Phe Lys Ile Glu Ile Glu Ala Met
 420 425 430

Ile Lys Lys Tyr Val Thr Lys Val Cys Pro
 435 440

<210> 38
 <211> 1326
 <212> DNA
 <213> *Taxus canadensis*

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<220>
<221> CDS
<222> (1)..(1326)
<223> coding sequence

<400> 38
atg gag aag gca ggc tca aca gac ttc cat gta aag aaa ttt gat cca      48
Met Glu Lys Ala Gly Ser Thr Asp Phe His Val Lys Lys Phe Asp Pro
1 5 10 15

gtc atg gta gcc cca agc ctt cca tcg ccc aaa gct acc gtc cag ctc      96
Val Met Val Ala Pro Ser Leu Pro Ser Pro Lys Ala Thr Val Gln Leu
20 25 30

tct gtc gtt gat agc cta aca atc tgc agg gga att ttt aac acg ttg      144
Ser Val Val Asp Ser Leu Thr Ile Cys Arg Gly Ile Phe Asn Thr Leu
35 40 45

ttg gtt ttc aat gcc cct gac aac att tct gca gat cct gta aaa ata      192
Leu Val Phe Asn Ala Pro Asp Asn Ile Ser Ala Asp Pro Val Lys Ile
50 55 60

att aga gag gct ctc tcc aag gtg ttg gtg tat tat ttc cct ctt gct      240
Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Phe Pro Leu Ala
65 70 75 80

ggg cgg ctc aga agt aaa gaa att ggg gaa ctt gaa gtg gag tgc aca      288
Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu Glu Val Glu Cys Thr
85 90 95

ggg gat ggt gct ctg ttt gtg gaa gcc atg gtg gaa gac acc att tca      336
Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val Glu Asp Thr Ile Ser
100 105 110

gtc tta cga gat ctg gat gac ctc aat cca tca ttt cag cag tta gtt      384
Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser Phe Gln Gln Leu Val
115 120 125

ttt tgg cat cca ttg gac act gct att gag gat ctt cat ctt gtg att      432
Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp Leu His Leu Val Ile
130 135 140

gtt cag gta aca cgt ttt aca tgt ggg ggc att gcc gtt gga gtg act      480
Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile Ala Val Gly Val Thr
145 150 155 160

ttg ccc cat agt gta tgt gat gga cgt gga gca gcc cag ttt gtt aca      528
Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Val Thr
165 170 175

gca ctg gca gag atg gcg agg gga gag gtt aag ccc tca cta gaa cca      576
Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Leu Glu Pro
180 185 190

ata tgg aat aga gaa ttg ttg aac cct gaa gac cct cta cat ctc cag      624
Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp Pro Leu His Leu Gln
195 200 205

tta aat caa ttt gat tcg ata tgc cca cct cca atg ctg gag gaa ttg      672

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Leu	Asn	Gln	Phe	Asp	Ser	Ile	Cys	Pro	Pro	Pro	Met	Leu	Glu	Glu	Leu	
210						215					220					
ggg	caa	gct	tct	ttt	gtt	ata	aac	gtt	gac	acc	ata	gaa	tat	atg	aag	720
Gly	Gln	Ala	Ser	Phe	Val	Ile	Asn	Val	Asp	Thr	Ile	Glu	Tyr	Met	Lys	
225					230				235						240	
caa	tgt	gtc	atg	gag	gaa	tgt	aat	gaa	ttt	tgt	tcg	tct	ttt	gaa	gta	768
Gln	Cys	Val	Met	Glu	Glu	Cys	Asn	Glu	Phe	Cys	Ser	Ser	Phe	Glu	Val	
				245				250						255		
gtg	gca	gca	ttg	gtt	tgg	ata	gca	cgg	aca	aag	gct	ctt	caa	att	cca	816
Val	Ala	Ala	Leu	Val	Trp	Ile	Ala	Arg	Thr	Lys	Ala	Leu	Gln	Ile	Pro	
			260				265						270			
cat	act	gag	aat	gtg	aag	ctt	ctc	ttt	gcg	atg	gat	ttg	agg	aaa	tta	864
His	Thr	Glu	Asn	Val	Lys	Leu	Leu	Phe	Ala	Met	Asp	Leu	Arg	Lys	Leu	
		275				280						285				
ttt	aat	ccc	cca	ctt	cca	aat	gga	tat	tat	ggg	aat	gcc	att	ggg	act	912
Phe	Asn	Pro	Pro	Leu	Pro	Asn	Gly	Tyr	Tyr	Gly	Asn	Ala	Ile	Gly	Thr	
	290					295					300					
gca	tat	gca	atg	gat	aat	gtc	caa	gac	ctc	tta	aat	gga	tct	ctt	ttg	960
Ala	Tyr	Ala	Met	Asp	Asn	Val	Gln	Asp	Leu	Leu	Asn	Gly	Ser	Leu	Leu	
305					310				315						320	
cgt	gct	ata	atg	att	ata	aaa	aaa	gca	aag	gct	gat	tta	aaa	gat	aat	1008
Arg	Ala	Ile	Met	Ile	Ile	Lys	Lys	Ala	Lys	Ala	Asp	Leu	Lys	Asp	Asn	
				325				330						335		
tat	tcg	agg	tca	agg	gta	gtt	aca	aac	cca	tat	tca	tta	gat	gtg	aac	1056
Tyr	Ser	Arg	Ser	Arg	Val	Val	Thr	Asn	Pro	Tyr	Ser	Leu	Asp	Val	Asn	
			340				345						350			
aag	aaa	tcc	gac	aac	att	ctt	gca	ttg	agt	gac	tgg	agg	cgg	ttg	gga	1104
Lys	Lys	Ser	Asp	Asn	Ile	Leu	Ala	Leu	Ser	Asp	Trp	Arg	Arg	Leu	Gly	
		355					360					365				
ttt	tat	gaa	gcc	gat	ttt	ggg	tgg	gga	ggg	cca	ctg	aat	gta	agt	tcc	1152
Phe	Tyr	Glu	Ala	Asp	Phe	Gly	Trp	Gly	Gly	Pro	Leu	Asn	Val	Ser	Ser	
	370					375					380					
ctg	caa	cgg	ttg	gaa	aat	gga	ttg	cct	atg	ttt	agt	act	ttt	cta	tac	1200
Leu	Gln	Arg	Leu	Glu	Asn	Gly	Leu	Pro	Met	Phe	Ser	Thr	Phe	Leu	Tyr	
385					390				395						400	
cta	cta	cct	gcc	aaa	aac	aag	tct	gat	gga	atc	aag	ctg	cta	ctg	tct	1248
Leu	Leu	Pro	Ala	Lys	Asn	Lys	Ser	Asp	Gly	Ile	Lys	Leu	Leu	Leu	Ser	
			405					410						415		
tgt	atg	cca	cca	aca	aca	ttg	aaa	tca	ttt	aaa	att	gta	atg	gaa	gct	1296
Cys	Met	Pro	Pro	Thr	Thr	Leu	Lys	Ser	Phe	Lys	Ile	Val	Met	Glu	Ala	
			420					425				430				
atg	ata	gag	aaa	tat	gta	agt	aaa	gtg	tga							1326
Met	Ile	Glu	Lys	Tyr	Val	Ser	Lys	Val								
		435					440									

<210> 39

<211> 441
 <212> PRT
 <213> Taxus canadensis

<400> 39

Met Glu Lys Ala Gly Ser Thr Asp Phe His Val Lys Lys Phe Asp Pro
 1 5 10 15

Val Met Val Ala Pro Ser Leu Pro Ser Pro Lys Ala Thr Val Gln Leu
 20 25 30

Ser Val Val Asp Ser Leu Thr Ile Cys Arg Gly Ile Phe Asn Thr Leu
 35 40 45

Leu Val Phe Asn Ala Pro Asp Asn Ile Ser Ala Asp Pro Val Lys Ile
 50 55 60

Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Phe Pro Leu Ala
 65 70 75 80

Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95

Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val Glu Asp Thr Ile Ser
 100 105 110

Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser Phe Gln Gln Leu Val
 115 120 125

Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp Leu His Leu Val Ile
 130 135 140

Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile Ala Val Gly Val Thr
 145 150 155 160

Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Val Thr
 165 170 175

Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Leu Glu Pro
 180 185 190

Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp Pro Leu His Leu Gln
 195 200 205

Leu Asn Gln Phe Asp Ser Ile Cys Pro Pro Pro Met Leu Glu Glu Leu
 210 215 220

Gly Gln Ala Ser Phe Val Ile Asn Val Asp Thr Ile Glu Tyr Met Lys
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Gln Cys Val Met Glu Glu Cys Asn Glu Phe Cys Ser Ser Phe Glu Val
 245 250 255

Val Ala Ala Leu Val Trp Ile Ala Arg Thr Lys Ala Leu Gln Ile Pro
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His Thr Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Lys Leu
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Phe Asn Pro Pro Leu Pro Asn Gly Tyr Tyr Gly Asn Ala Ile Gly Thr
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Ala Tyr Ala Met Asp Asn Val Gln Asp Leu Leu Asn Gly Ser Leu Leu
 305 310 315 320

Arg Ala Ile Met Ile Ile Lys Lys Ala Lys Ala Asp Leu Lys Asp Asn
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Tyr Ser Arg Ser Arg Val Val Thr Asn Pro Tyr Ser Leu Asp Val Asn
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Lys Lys Ser Asp Asn Ile Leu Ala Leu Ser Asp Trp Arg Arg Leu Gly
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Phe Tyr Glu Ala Asp Phe Gly Trp Gly Gly Pro Leu Asn Val Ser Ser
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Leu Gln Arg Leu Glu Asn Gly Leu Pro Met Phe Ser Thr Phe Leu Tyr
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Leu Leu Pro Ala Lys Asn Lys Ser Asp Gly Ile Lys Leu Leu Leu Ser
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cta cag tcc tct gct att ctt ctc act gtt gtt tct gga atc atc gtc      96
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cct ccg ggg aaa tta ggc ctc cct ctc att ggg gaa tcg tta tca ttc      192
Pro Pro Gly Lys Leu Gly Leu Pro Leu Ile Gly Glu Ser Leu Ser Phe
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gtg aag aaa tac ggc aat gtc ttc aag aca tcg tta ctt ggg caa ccc      288
Val Lys Lys Tyr Gly Asn Val Phe Lys Thr Ser Leu Leu Gly Gln Pro
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aca gta gta ctg tgt ggc gca gcc gga aac cgc cta att ctg tcg aac      336
Thr Val Val Leu Cys Gly Ala Ala Gly Asn Arg Leu Ile Leu Ser Asn
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cag gag aag ctg ttg agc cga acg gtg tcg gat cga gta gcg aaa ctg      384
Gln Glu Lys Leu Leu Ser Arg Thr Val Ser Asp Arg Val Ala Lys Leu
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acg ggt gat act tct att tcg gtt ata gcg gga gac agt cat cgc atc      432
Thr Gly Asp Thr Ser Ile Ser Val Ile Ala Gly Asp Ser His Arg Ile
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cac att ggc gaa atg agc gca cat atc cga aat cat atc aac caa gta      528
His Ile Gly Glu Met Ser Ala His Ile Arg Asn His Ile Asn Gln Val
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tgg aag gga aaa gat gaa gtg aac gtg ctt agt ttg gca aga gag ctg      576
Trp Lys Gly Lys Asp Glu Val Asn Val Leu Ser Leu Ala Arg Glu Leu
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gtc ttc gcc atg tcg gcc agt ttg ttt tta aat ata aat gat aga gag      624
Val Phe Ala Met Ser Ala Ser Leu Phe Leu Asn Ile Asn Asp Arg Glu
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gaa cag cac caa ttg cat aag act ctc gaa act att ctt ccc gga tat      672

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Glu	Gly	Asn	Ser	Lys	Arg	Arg	Lys	His	Phe	Ser	Val	Leu	Gln	Glu	Lys	
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Asp	Glu	Glu	Val	Leu	Asp	Asn	Ile	Ser	Ala	Leu	Ile	Asp	Gly	Ser	Tyr	
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Pro	Val	Phe	Gly	Pro	Arg	Gly	Lys	Ala	Ile	Thr	Asp	Ile	His	Tyr	Asp	
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Gly	Tyr	Thr	Ile	Pro	Lys	Gly	Trp	Gln	Leu	Ser	Trp	Ala	Thr	Tyr	Ser	
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Thr	His	Gln	Asn	Asp	Thr	Tyr	Phe	Asn	Glu	Pro	Asp	Lys	Phe	Met	Pro	
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Ser	Arg	Phe	Asp	Glu	Glu	Gly	Gly	Arg	Leu	Ala	Pro	Tyr	Thr	Phe	Val	
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Pro	Phe	Gly	Gly	Gly	Arg	Arg	Lys	Cys	Pro	Gly	Trp	Glu	Phe	Ala	Lys	
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Tyr Thr Pro Ile Asp Pro His Glu Ser Ile Trp Gly Arg Pro Leu Pro			
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cct gtc cct gcc aat gga ttt cct att aaa ctt att tct cga tcc taa			1488
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Ile Val Ile Leu Leu Leu Arg Ser Lys Arg Arg Ser Ser Leu Lys Leu			
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Pro Pro Gly Lys Leu Gly Leu Pro Leu Ile Gly Glu Ser Leu Ser Phe			
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Leu Trp Ala Leu Arg Ser Asn Thr Leu Glu Gln Phe Val Asp Lys Arg			
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Val Lys Lys Tyr Gly Asn Val Phe Lys Thr Ser Leu Leu Gly Gln Pro			
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Gln Glu Lys Leu Leu Ser Arg Thr Val Ser Asp Arg Val Ala Lys Leu			
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Thr Gly Asp Thr Ser Ile Ser Val Ile Ala Gly Asp Ser His Arg Ile			
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Ile Arg Ala Ala Val Ala Gly Phe Leu Gly Pro Ala Gly Leu Lys Ile			
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His Ile Gly Glu Met Ser Ala His Ile Arg Asn His Ile Asn Gln Val			
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Val Phe Ala Met Ser Ala Ser Leu Phe Leu Asn Ile Asn Asp Arg Glu
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Glu Gln His Gln Leu His Lys Thr Leu Glu Thr Ile Leu Pro Gly Tyr
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Phe Ser Val Pro Ile Asn Phe Pro Gly Phe Ala Phe Arg Lys Ala Leu
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Glu Gly Asn Ser Lys Arg Arg Lys His Phe Ser Val Leu Gln Glu Lys
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Arg Arg Arg Asp Leu Ser Val Gly Leu Ala Ser Arg Thr Gln Asp Leu
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Leu Ser Val Leu Leu Ala Tyr Glu Asp Asp Lys Gly Asn Pro Leu Thr
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Asp Glu Glu Val Leu Asp Asn Ile Ser Ala Leu Ile Asp Gly Ser Tyr
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Glu Ser Thr Ser Ser Gln Met Ala Met Leu Leu Lys Leu Leu Ser Asp
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His Pro Glu Cys Tyr Glu Lys Val Val Gln Glu Gln Leu Glu Ile Ala
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Ser His Lys Lys Glu Gly Glu Glu Ile Thr Trp Lys Asp Val Lys Ala
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Met Arg Tyr Thr Trp Gln Val Met Gln Glu Thr Leu Arg Met Phe Ala
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Thr His Gln Asn Asp Thr Tyr Phe Asn Glu Pro Asp Lys Phe Met Pro
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Ser Arg Phe Asp Glu Glu Gly Gly Arg Leu Ala Pro Tyr Thr Phe Val
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Pro Phe Gly Gly Gly Arg Arg Lys Cys Pro Gly Trp Glu Phe Ala Lys
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450 455 460

Tyr Thr Pro Ile Asp Pro His Glu Ser Ile Trp Gly Arg Pro Leu Pro
465 470 475 480

Pro Val Pro Ala Asn Gly Phe Pro Ile Lys Leu Ile Ser Arg Ser
485 490 495